

# SEQUENCE LISTING

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<110>  Elich, Tedd D.
        Volrath, Sandra L.
        Weatherly, Stephanie C.

<120>  RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
        ACETYL CoA CARBOXYLASE INHIBITORS

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<150>  US 60/401,170
<151>  2003-08-05

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<170>  PatentIn version 3.2

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Tyr Val Arg Leu Gln Lys Gly Thr Arg Pro Ile Thr Ser Val Leu Ile  
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Glu Tyr Val Asn Ala Gly Thr Val Glu Tyr Leu Phe Ser Glu Leu Pro  
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Gln Val Glu His Pro Val Thr Glu Met Ile Thr His Val Asn Leu Pro  
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Asp Val Arg Arg Leu Tyr Asn Lys Asp Ala Phe Glu Thr Thr Val Ile  
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Asp Phe Asp Ala Glu Lys Gln Lys Pro Pro His Gly His Val Ile Ala  
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Ala Arg Ile Thr Ala Glu Asp Pro Asn Ala Gly Phe Gln Pro Thr Ser  
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Tyr Phe Ser Val Asp Ser Ser Gly Gln Val His Glu Phe Ala Asp Ser  
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His Thr Thr Val Glu Tyr Ile Val Asn Met Met Glu Ser Asp Asp Phe  
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 cta gag aat gcc cct ccg tcc aag gtc aag gag tgg gtt gcc gca cac 192  
 Leu Glu Asn Ala Pro Pro Ser Lys Val Lys Glu Trp Val Ala Ala His  
 50 55 60  
 gac ggc cac aca gtc atc acc aac gtc ctg att gcc aac aac ggt atc 240  
 Asp Gly His Thr Val Ile Thr Asn Val Leu Ile Ala Asn Asn Gly Ile  
 65 70 75 80  
 gct gcc gtc aag gag att cga tcc gtg cga aaa tgg gca tac gag acg 288  
 Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr  
 85 90 95  
 ttc gga gac gaa agg gcc att cag ttc act gtg atg gcc act ccc gag 336  
 Phe Gly Asp Glu Arg Ala Ile Gln Phe Thr Val Met Ala Thr Pro Glu  
 100 105 110  
 gat ttg caa gca aac gca gac tac att cgc atg gca gac cac tac gtc 384  
 Asp Leu Gln Ala Asn Ala Asp Tyr Ile Arg Met Ala Asp His Tyr Val  
 115 120 125  
 gag gtc cct ggt ggt aca aac aac aac aac tat gcg aac gtc gag ttg 432  
 Glu Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu  
 130 135 140  
 atc gtc gat gtt gcg gag cgc atg aac gtg cac gcc gtt tgg gcc ggt 480  
 Ile Val Asp Val Ala Glu Arg Met Asn Val His Ala Val Trp Ala Gly  
 145 150 155 160  
 tgg gga cac gca tcg gag aac cca aag ctc cct gag tct ctc gct gcc 528

Trp	Gly	His	Ala	Ser	Glu	Asn	Pro	Lys	Leu	Pro	Glu	Ser	Leu	Ala	Ala		
				165					170					175			
tcg	cct	aag	aaa	att	att	ttc	atc	ggc	cct	ccc	ggc	tcc	gcg	atg	cgc		576
Ser	Pro	Lys	Lys	Ile	Ile	Phe	Ile	Gly	Pro	Pro	Gly	Ser	Ala	Met	Arg		
			180					185					190				
tcg	ctc	ggt	gac	aag	atc	tct	tct	acc	att	gtc	gct	caa	cat	gcc	cag		624
Ser	Leu	Gly	Asp	Lys	Ile	Ser	Ser	Thr	Ile	Val	Ala	Gln	His	Ala	Gln		
		195					200					205					
gtc	cca	tgt	atc	ccc	tgg	tcg	gga	act	ggt	gtt	gat	gcg	gtc	caa	atc		672
Val	Pro	Cys	Ile	Pro	Trp	Ser	Gly	Thr	Gly	Val	Asp	Ala	Val	Gln	Ile		
	210					215					220						
gac	aag	aag	gga	att	gtc	acc	gtc	gac	gac	gac	act	tat	gcc	aaa	gga		720
Asp	Lys	Lys	Gly	Ile	Val	Thr	Val	Asp	Asp	Asp	Thr	Tyr	Ala	Lys	Gly		
225					230					235					240		
tgc	gtc	act	tca	tgg	cag	gag	ggt	ctt	gag	aag	gcc	aga	caa	att	ggt		768
Cys	Val	Thr	Ser	Trp	Gln	Glu	Gly	Leu	Glu	Lys	Ala	Arg	Gln	Ile	Gly		
				245					250					255			
ttc	ccg	gtc	atg	atc	aag	gct	tct	gag	ggt	ggt	ggt	ggc	aag	ggt	atc		816
Phe	Pro	Val	Met	Ile	Lys	Ala	Ser	Glu	Gly	Gly	Gly	Gly	Lys	Gly	Ile		
			260					265					270				
cgt	aag	gct	gtc	tcc	gag	gag	ggc	ttc	gag	gag	ctc	tac	aag	gcc	gct		864
Arg	Lys	Ala	Val	Ser	Glu	Glu	Gly	Phe	Glu	Glu	Leu	Tyr	Lys	Ala	Ala		
		275					280					285					
gcc	agt	gaa	atc	ccc	ggt	tcg	ccc	atc	ttc	atc	atg	aag	ctt	gca	ggc		912
Ala	Ser	Glu	Ile	Pro	Gly	Ser	Pro	Ile	Phe	Ile	Met	Lys	Leu	Ala	Gly		
	290					295					300						
aac	gcc	agg	cat	ttg	gaa	gtg	cag	ctt	ctc	gct	gat	cag	tac	ggc	aac		960
Asn	Ala	Arg	His	Leu	Glu	Val	Gln	Leu	Leu	Ala	Asp	Gln	Tyr	Gly	Asn		
305					310					315				320			
aac	atc	tcc	ctc	ttt	ggt	cgt	gat	tgt	tcc	gtc	cag	cga	agg	cac	caa		1008
Asn	Ile	Ser	Leu	Phe	Gly	Arg	Asp	Cys	Ser	Val	Gln	Arg	Arg	His	Gln		
				325					330					335			
aag	att	atc	gag	gaa	gct	ccc	gtg	acc	atc	gcc	aag	ccc	gac	acg	ttc		1056
Lys	Ile	Ile	Glu	Glu	Ala	Pro	Val	Thr	Ile	Ala	Lys	Pro	Asp	Thr	Phe		
			340					345					350				
aag	gcc	atg	gag	gag	gcc	gct	gtt	cgt	ctt	ggt	cgt	ctt	gtc	ggt	tac		1104
Lys	Ala	Met	Glu	Glu	Ala	Ala	Val	Arg	Leu	Gly	Arg	Leu	Val	Gly	Tyr		
		355					360					365					
gtc	tct	gct	ggt	acc	gtc	gag	tac	ctg	tac	tcg	cac	gcc	gac	gac	aag		1152
Val	Ser	Ala	Gly	Thr	Val	Glu	Tyr	Leu	Tyr	Ser	His	Ala	Asp	Asp	Lys		
		370				375					380						
ttc	tac	ttc	ctg	gag	ctc	aac	cct	cgt	ctt	cag	gtc	gag	cat	cct	acc		1200
Phe	Tyr	Phe	Leu	Glu	Leu	Asn	Pro	Arg	Leu	Gln	Val	Glu	His	Pro	Thr		
	385				390					395					400		
act	gag	ggt	gtc	agt	ggt	gtc	aac	ctc	ccc	gct	tcg	cag	ctt	cag	att		1248
Thr	Glu	Gly	Val	Ser	Gly	Val	Asn	Leu	Pro	Ala	Ser	Gln	Leu	Gln	Ile		

405										410					415					
gcc	atg	ggt	atc	cct	ctc	cac	agg	ata	tct	gac	att	agg	ctc	ctt	tac	1296				
Ala	Met	Gly	Ile	Pro	Leu	His	Arg	Ile	Ser	Asp	Ile	Arg	Leu	Leu	Tyr					
			420					425					430							
ggt	gtg	gac	ccc	aag	ctc	tcg	act	gag	atc	gac	ttt	gac	ttc	aag	aac	1344				
Gly	Val	Asp	Pro	Lys	Leu	Ser	Thr	Glu	Ile	Asp	Phe	Asp	Phe	Lys	Asn					
			435				440					445								
ccc	gac	agc	gag	aag	acg	cag	agg	agg	cca	tcg	ccc	aaa	ggc	cac	ctt	1392				
Pro	Asp	Ser	Glu	Lys	Thr	Gln	Arg	Arg	Pro	Ser	Pro	Lys	Gly	His	Leu					
	450					455					460									
act	gcc	tgc	cgt	att	acc	tca	gag	gac	cct	gga	gag	ggc	ttc	aag	ccg	1440				
Thr	Ala	Cys	Arg	Ile	Thr	Ser	Glu	Asp	Pro	Gly	Glu	Gly	Phe	Lys	Pro					
465					470				475						480					
tcc	aac	ggt	gtc	atg	cac	gag	ctg	aac	ttc	cgc	agt	agt	tca	aac	gtg	1488				
Ser	Asn	Gly	Val	Met	His	Glu	Leu	Asn	Phe	Arg	Ser	Ser	Ser	Asn	Val					
				485				490						495						
tgg	ggt	tac	ttc	tca	gtc	ggt	acg	cag	ggt	gga	att	cac	agt	ttc	tcc	1536				
Trp	Gly	Tyr	Phe	Ser	Val	Gly	Thr	Gln	Gly	Gly	Ile	His	Ser	Phe	Ser					
			500					505					510							
gac	agt	cag	ttc	ggt	cac	att	ttc	gcc	tat	ggc	gag	aac	cga	tcc	gcg	1584				
Asp	Ser	Gln	Phe	Gly	His	Ile	Phe	Ala	Tyr	Gly	Glu	Asn	Arg	Ser	Ala					
		515					520					525								
tca	agg	aag	cac	atg	gtt	atc	gcc	ttg	aag	gaa	ctt	agc	att	cgt	ggt	1632				
Ser	Arg	Lys	His	Met	Val	Ile	Ala	Leu	Lys	Glu	Leu	Ser	Ile	Arg	Gly					
	530					535				540										
gat	ttc	cgc	acc	acg	gtc	gag	tac	cta	atc	aag	ctt	ctg	gag	acg	gag	1680				
Asp	Phe	Arg	Thr	Thr	Val	Glu	Tyr	Leu	Ile	Lys	Leu	Leu	Glu	Thr	Glu					
545					550					555					560					
gct	ttc	gag	gag	aac	acc	att	acc	act	ggc	tgg	ctg	gac	gag	ctt	att	1728				
Ala	Phe	Glu	Glu	Asn	Thr	Ile	Thr	Thr	Gly	Trp	Leu	Asp	Glu	Leu	Ile					
				565				570					575							
tcg	aag	aag	ctc	act	gcg	gag	agg	ccc	gac	aag	atg	ctt	gct	gtt		1773				
Ser	Lys	Lys	Leu	Thr	Ala	Glu	Arg	Pro	Asp	Lys	Met	Leu	Ala	Val						
			580				585					590								

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 <213> Magnaporthe grisea

<400> 6

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Asn	Gly	Ala	Asn	Gly	Val	Thr	Val	Pro	Val	Ala	Asn	Gly	Lys	Ala	Thr
			20					25					30		

Tyr Ala Gln Arg His Lys Ile Ala Asp His Phe Ile Gly Gly Asn Arg  
 35 40 45  
 Leu Glu Asn Ala Pro Pro Ser Lys Val Lys Glu Trp Val Ala Ala His  
 50 55 60  
 Asp Gly His Thr Val Ile Thr Asn Val Leu Ile Ala Asn Asn Gly Ile  
 65 70 75 80  
 Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr  
 85 90 95  
 Phe Gly Asp Glu Arg Ala Ile Gln Phe Thr Val Met Ala Thr Pro Glu  
 100 105 110  
 Asp Leu Gln Ala Asn Ala Asp Tyr Ile Arg Met Ala Asp His Tyr Val  
 115 120 125  
 Glu Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu  
 130 135 140  
 Ile Val Asp Val Ala Glu Arg Met Asn Val His Ala Val Trp Ala Gly  
 145 150 155 160  
 Trp Gly His Ala Ser Glu Asn Pro Lys Leu Pro Glu Ser Leu Ala Ala  
 165 170 175  
 Ser Pro Lys Lys Ile Ile Phe Ile Gly Pro Pro Gly Ser Ala Met Arg  
 180 185 190  
 Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln His Ala Gln  
 195 200 205  
 Val Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp Ala Val Gln Ile  
 210 215 220  
 Asp Lys Lys Gly Ile Val Thr Val Asp Asp Asp Thr Tyr Ala Lys Gly  
 225 230 235 240  
 Cys Val Thr Ser Trp Gln Glu Gly Leu Glu Lys Ala Arg Gln Ile Gly  
 245 250 255  
 Phe Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile  
 260 265 270

Arg Lys Ala Val Ser Glu Glu Gly Phe Glu Glu Leu Tyr Lys Ala Ala  
 275 280 285

Ala Ser Glu Ile Pro Gly Ser Pro Ile Phe Ile Met Lys Leu Ala Gly  
 290 295 300

Asn Ala Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn  
 305 310 315 320

Asn Ile Ser Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln  
 325 330 335

Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala Lys Pro Asp Thr Phe  
 340 345 350

Lys Ala Met Glu Glu Ala Ala Val Arg Leu Gly Arg Leu Val Gly Tyr  
 355 360 365

Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser His Ala Asp Asp Lys  
 370 375 380

Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr  
 385 390 395 400

Thr Glu Gly Val Ser Gly Val Asn Leu Pro Ala Ser Gln Leu Gln Ile  
 405 410 415

Ala Met Gly Ile Pro Leu His Arg Ile Ser Asp Ile Arg Leu Leu Tyr  
 420 425 430

Gly Val Asp Pro Lys Leu Ser Thr Glu Ile Asp Phe Asp Phe Lys Asn  
 435 440 445

Pro Asp Ser Glu Lys Thr Gln Arg Arg Pro Ser Pro Lys Gly His Leu  
 450 455 460

Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Gly Glu Gly Phe Lys Pro  
 465 470 475 480

Ser Asn Gly Val Met His Glu Leu Asn Phe Arg Ser Ser Ser Asn Val  
 485 490 495

Trp Gly Tyr Phe Ser Val Gly Thr Gln Gly Gly Ile His Ser Phe Ser  
 500 505 510

Asp Ser Gln Phe Gly His Ile Phe Ala Tyr Gly Glu Asn Arg Ser Ala

515	520	525	
Ser Arg Lys His Met Val Ile Ala Leu Lys Glu Leu Ser Ile Arg Gly			
530	535	540	
Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu			
545	550	555	560
Ala Phe Glu Glu Asn Thr Ile Thr Thr Gly Trp Leu Asp Glu Leu Ile			
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Ser Lys Lys Leu Thr Ala Glu Arg Pro Asp Lys Met Leu Ala Val			
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Ser Glu Glu Ser Leu Phe Glu Ser Ser Pro Gln Lys Met Glu Tyr Glu			
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att aca aac tac tca gaa aga cat aca gaa ctt cca ggt cat ttc att			96
Ile Thr Asn Tyr Ser Glu Arg His Thr Glu Leu Pro Gly His Phe Ile			
20	25	30	
ggc ctc aat aca gta gat aaa cta gag gag tcc ccg tta agg gac ttt			144
Gly Leu Asn Thr Val Asp Lys Leu Glu Glu Ser Pro Leu Arg Asp Phe			
35	40	45	
gtt aag agt cac ggt ggt cac acg gtc ata tcc aag atc ctg ata gca			192
Val Lys Ser His Gly Gly His Thr Val Ile Ser Lys Ile Leu Ile Ala			
50	55	60	
aat aat ggt att gcc gcc gtg aaa gaa att aga tcc gtc aga aaa tgg			240
Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp			
65	70	75	80
gca tac gag acg ttc ggc gat gac aga acc gtc caa ttc gtc gcc atg			288
Ala Tyr Glu Thr Phe Gly Asp Asp Arg Thr Val Gln Phe Val Ala Met			
85	90	95	



gcc acc cca gaa gat ctg gag gcc aac gca gaa tat atc cgt atg gcc Ala Thr Pro Glu Asp Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met Ala 100 105 110	336
gat caa tac att gaa gtg cca ggt ggt act aat aat aac aac tac gct Asp Gln Tyr Ile Glu Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala 115 120 125	384
aac gta gac ttg atc gta gac atc gcc gaa aga gca gac gta gac gcc Asn Val Asp Leu Ile Val Asp Ile Ala Glu Arg Ala Asp Val Asp Ala 130 135 140	432
gta tgg gct ggc tgg ggt cac gcc tcc gag aat cca cta ttg cct gaa Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro Glu 145 150 155 160	480
aaa ttg tcc cag tct aag agg aaa gtc atc ttt att ggg cct cca ggt Lys Leu Ser Gln Ser Lys Arg Lys Val Ile Phe Ile Gly Pro Pro Gly 165 170 175	528
aac gcc atg agg tct tta ggt gat aaa atc tcc tct acc att gtc gct Asn Ala Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala 180 185 190	576
caa agt gct aaa gtc cca tgt att cca tgg tct ggt acc ggt gtt gac Gln Ser Ala Lys Val Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp 195 200 205	624
acc gtt cac gtg gac gag aaa acc ggt ctg gtc tct gtc gac gat gac Thr Val His Val Asp Glu Lys Thr Gly Leu Val Ser Val Asp Asp Asp 210 215 220	672
atc tat caa aag ggt tgt tgt acc tct cct gaa gat ggt tta caa aag Ile Tyr Gln Lys Gly Cys Cys Thr Ser Pro Glu Asp Gly Leu Gln Lys 225 230 235 240	720
gcc aag cgt att ggt ttt cct gtc atg att aag gca tcc gaa ggt ggt Ala Lys Arg Ile Gly Phe Pro Val Met Ile Lys Ala Ser Glu Gly Gly 245 250 255	768
ggt ggt aaa ggt atc aga caa gtt gaa cgt gaa gaa gat ttc atc gct Gly Gly Lys Gly Ile Arg Gln Val Glu Arg Glu Glu Asp Phe Ile Ala 260 265 270	816
tta tac cac cag gca gcc aac gaa att cca ggc tcc ccc att ttc atc Leu Tyr His Gln Ala Ala Asn Glu Ile Pro Gly Ser Pro Ile Phe Ile 275 280 285	864
atg aag ttg gcc ggt aga gcg cgt cac ttg gaa gtt caa ctg cta gca Met Lys Leu Ala Gly Arg Ala Arg His Leu Glu Val Gln Leu Leu Ala 290 295 300	912
gat cag tac ggt aca aat att tcc ttg ttc ggt aga gac tgt tcc gtt Asp Gln Tyr Gly Thr Asn Ile Ser Leu Phe Gly Arg Asp Cys Ser Val 305 310 315 320	960
cag aga cgt cat caa aaa att atc gaa gaa gca cca gtt aca att gcc Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala 325 330 335	1008
aag gct gaa aca ttt cac gag atg gaa aag gct gcc gtc aga ctg ggg	1056

Lys	Ala	Glu	Thr	Phe	His	Glu	Met	Glu	Lys	Ala	Ala	Val	Arg	Leu	Gly		
			340					345					350				
aaa	cta	gtc	ggg	tat	gtc	tct	gcc	ggg	acc	gtg	gag	tat	cta	tat	tct	1104	
Lys	Leu	Val	Gly	Tyr	Val	Ser	Ala	Gly	Thr	Val	Glu	Tyr	Leu	Tyr	Ser		
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cat	gat	gat	gga	aaa	ttc	tac	ttt	tta	gaa	ttg	aac	cca	aga	tta	caa	1152	
His	Asp	Asp	Gly	Lys	Phe	Tyr	Phe	Leu	Glu	Leu	Asn	Pro	Arg	Leu	Gln		
	370					375					380						
gtc	gag	cat	cca	aca	acg	gaa	atg	gtc	tcc	ggg	gtt	aac	tta	cct	gca	1200	
Val	Glu	His	Pro	Thr	Thr	Glu	Met	Val	Ser	Gly	Val	Asn	Leu	Pro	Ala		
	385				390					395					400		
gct	caa	tta	caa	atc	gct	atg	ggg	atc	cct	atg	cat	aga	ata	agt	gac	1248	
Ala	Gln	Leu	Gln	Ile	Ala	Met	Gly	Ile	Pro	Met	His	Arg	Ile	Ser	Asp		
				405				410						415			
att	aga	act	tta	tat	ggg	atg	aat	cct	cat	tct	gcc	tca	gaa	atc	gat	1296	
Ile	Arg	Thr	Leu	Tyr	Gly	Met	Asn	Pro	His	Ser	Ala	Ser	Glu	Ile	Asp		
			420					425					430				
ttc	gaa	ttc	aaa	act	caa	gat	gcc	acc	aag	aaa	caa	aga	aga	cct	att	1344	
Phe	Glu	Phe	Lys	Thr	Gln	Asp	Ala	Thr	Lys	Lys	Gln	Arg	Arg	Pro	Ile		
		435					440					445					
cca	aag	ggg	cat	tgt	acc	gct	tgt	cgt	atc	aca	tca	gaa	gat	cca	aac	1392	
Pro	Lys	Gly	His	Cys	Thr	Ala	Cys	Arg	Ile	Thr	Ser	Glu	Asp	Pro	Asn		
	450					455					460						
gat	gga	ttc	aag	cca	tcg	ggg	ggg	act	ttg	cat	gaa	cta	aac	ttc	cgt	1440	
Asp	Gly	Phe	Lys	Pro	Ser	Gly	Gly	Thr	Leu	His	Glu	Leu	Asn	Phe	Arg		
	465				470				475					480			
tct	tcc	tct	aat	gtt	tgg	ggg	tac	ttc	tcc	gtg	ggg	aac	aat	ggg	aat	1488	
Ser	Ser	Ser	Asn	Val	Trp	Gly	Tyr	Phe	Ser	Val	Gly	Asn	Asn	Gly	Asn		
			485					490						495			
att	cac	tcc	ttt	tcg	gac	tct	cag	ttc	ggc	cat	att	ttt	gct	ttt	ggg	1536	
Ile	His	Ser	Phe	Ser	Asp	Ser	Gln	Phe	Gly	His	Ile	Phe	Ala	Phe	Gly		
			500				505						510				
gaa	aat	aga	caa	gct	tcc	agg	aaa	cac	atg	gtt	gtt	gcc	ctg	aag	gaa	1584	
Glu	Asn	Arg	Gln	Ala	Ser	Arg	Lys	His	Met	Val	Val	Ala	Leu	Lys	Glu		
		515					520					525					
ttg	tcc	att	agg	ggg	gat	ttc	aga	act	act	gtg	gaa	tac	ttg	atc	aaa	1632	
Leu	Ser	Ile	Arg	Gly	Asp	Phe	Arg	Thr	Thr	Val	Glu	Tyr	Leu	Ile	Lys		
		530				535					540						
ctt	ttg	gaa	act	gaa	gat	ttc	gag	gat	aac	act	att	acc	acc	ggg	tgg	1680	
Leu	Leu	Glu	Thr	Glu	Asp	Phe	Glu	Asp	Asn	Thr	Ile	Thr	Thr	Gly	Trp		
				545		550				555					560		
ttg	gac	gat	ttg	att	act	cat	aaa	atg	acc	gct	gaa	aag	cct	gat	cca	1728	
Leu	Asp	Asp	Leu	Ile	Thr	His	Lys	Met	Thr	Ala	Glu	Lys	Pro	Asp	Pro		
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act	ctt	gcc	gtc													1740	
Thr	Leu	Ala	Val														

580

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<212> PRT  
<213> *Saccharomyces cerevisiae*

<400> 8

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Ile Thr Asn Tyr Ser Glu Arg His Thr Glu Leu Pro Gly His Phe Ile  
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Gly Leu Asn Thr Val Asp Lys Leu Glu Glu Ser Pro Leu Arg Asp Phe  
35 40 45

Val Lys Ser His Gly Gly His Thr Val Ile Ser Lys Ile Leu Ile Ala  
50 55 60

Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp  
65 70 75 80

Ala Tyr Glu Thr Phe Gly Asp Asp Arg Thr Val Gln Phe Val Ala Met  
85 90 95

Ala Thr Pro Glu Asp Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met Ala  
100 105 110

Asp Gln Tyr Ile Glu Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala  
115 120 125

Asn Val Asp Leu Ile Val Asp Ile Ala Glu Arg Ala Asp Val Asp Ala  
130 135 140

Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro Glu  
145 150 155 160

Lys Leu Ser Gln Ser Lys Arg Lys Val Ile Phe Ile Gly Pro Pro Gly  
165 170 175

Asn Ala Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala  
180 185 190

Gln Ser Ala Lys Val Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp  
195 200 205

Thr Val His Val Asp Glu Lys Thr Gly Leu Val Ser Val Asp Asp Asp  
 210 215 220

Ile Tyr Gln Lys Gly Cys Cys Thr Ser Pro Glu Asp Gly Leu Gln Lys  
 225 230 235 240

Ala Lys Arg Ile Gly Phe Pro Val Met Ile Lys Ala Ser Glu Gly Gly  
 245 250 255

Gly Gly Lys Gly Ile Arg Gln Val Glu Arg Glu Glu Asp Phe Ile Ala  
 260 265 270

Leu Tyr His Gln Ala Ala Asn Glu Ile Pro Gly Ser Pro Ile Phe Ile  
 275 280 285

Met Lys Leu Ala Gly Arg Ala Arg His Leu Glu Val Gln Leu Leu Ala  
 290 295 300

Asp Gln Tyr Gly Thr Asn Ile Ser Leu Phe Gly Arg Asp Cys Ser Val  
 305 310 315 320

Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala  
 325 330 335

Lys Ala Glu Thr Phe His Glu Met Glu Lys Ala Ala Val Arg Leu Gly  
 340 345 350

Lys Leu Val Gly Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser  
 355 360 365

His Asp Asp Gly Lys Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln  
 370 375 380

Val Glu His Pro Thr Thr Glu Met Val Ser Gly Val Asn Leu Pro Ala  
 385 390 395 400

Ala Gln Leu Gln Ile Ala Met Gly Ile Pro Met His Arg Ile Ser Asp  
 405 410 415

Ile Arg Thr Leu Tyr Gly Met Asn Pro His Ser Ala Ser Glu Ile Asp  
 420 425 430

Phe Glu Phe Lys Thr Gln Asp Ala Thr Lys Lys Gln Arg Arg Pro Ile  
 435 440 445

Pro Lys Gly His Cys Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Asn  
 450 455 460

Asp Gly Phe Lys Pro Ser Gly Gly Thr Leu His Glu Leu Asn Phe Arg  
 465 470 475 480

Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly Asn  
 485 490 495

Ile His Ser Phe Ser Asp Ser Gln Phe Gly His Ile Phe Ala Phe Gly  
 500 505 510

Glu Asn Arg Gln Ala Ser Arg Lys His Met Val Val Ala Leu Lys Glu  
 515 520 525

Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys  
 530 535 540

Leu Leu Glu Thr Glu Asp Phe Glu Asp Asn Thr Ile Thr Thr Gly Trp  
 545 550 555 560

Leu Asp Asp Leu Ile Thr His Lys Met Thr Ala Glu Lys Pro Asp Pro  
 565 570 575

Thr Leu Ala Val  
 580

<210> 9  
 <211> 1896  
 <212> DNA  
 <213> Homo sapiens

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 <223> Human ACCase1 (alpha) BC domain (aa 1-632)

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 Met Asp Glu Pro Ser Pro Leu Ala Gln Pro Leu Glu Leu Asn Gln His  
 1 5 10 15  
 tct cga ttc ata ata ggt tct gtg tct gaa gat aac tca gag gat gag 96  
 Ser Arg Phe Ile Gly Ser Val Ser Glu Asp Asn Ser Glu Asp Glu  
 20 25 30  
 atc agc aac ctg gtg aag ttg gac cta ctg gag gag aag gag ggc tcc 144  
 Ile Ser Asn Leu Val Lys Leu Asp Leu Leu Glu Glu Lys Glu Gly Ser  
 35 40 45  
 ttg tca cct gct tct gtt ggc tca gat aca ctc tct gat ttg ggg atc 192

Leu	Ser	Pro	Ala	Ser	Val	Gly	Ser	Asp	Thr	Leu	Ser	Asp	Leu	Gly	Ile		
50						55				60							
tct	agc	cta	cag	gat	ggc	ttg	gcc	ttg	cac	ata	agg	tcc	agc	atg	tct	240	
Ser	Ser	Leu	Gln	Asp	Gly	Leu	Ala	Leu	His	Ile	Arg	Ser	Ser	Met	Ser		
65					70				75					80			
ggc	ttg	cac	cta	gta	aag	cag	ggc	cga	gac	aga	aag	aaa	ata	gat	tct	288	
Gly	Leu	His	Leu	Val	Lys	Gln	Gly	Arg	Asp	Arg	Lys	Lys	Ile	Asp	Ser		
				85				90					95				
caa	cga	gat	ttc	act	gtg	gct	tct	cca	gca	gaa	ttt	gtt	act	cgc	ttt	336	
Gln	Arg	Asp	Phe	Thr	Val	Ala	Ser	Pro	Ala	Glu	Phe	Val	Thr	Arg	Phe		
			100					105					110				
ggg	gga	aat	aaa	gtg	att	gag	aag	ggt	ctt	att	gct	aac	aat	ggc	att	384	
Gly	Gly	Asn	Lys	Val	Ile	Glu	Lys	Val	Leu	Ile	Ala	Asn	Asn	Gly	Ile		
		115					120					125					
gca	gca	gtg	aaa	tgc	atg	cgg	tct	atc	cgt	agg	tgg	tct	tat	gaa	atg	432	
Ala	Ala	Val	Lys	Cys	Met	Arg	Ser	Ile	Arg	Arg	Trp	Ser	Tyr	Glu	Met		
		130				135					140						
ttt	cga	aat	gaa	cgt	gca	att	aga	ttc	gtt	gtc	atg	gtc	aca	cct	gaa	480	
Phe	Arg	Asn	Glu	Arg	Ala	Ile	Arg	Phe	Val	Val	Met	Val	Thr	Pro	Glu		
145					150				155					160			
gac	ctt	aaa	gcc	aat	gca	gaa	tac	att	aag	atg	gca	gat	cac	tat	gtg	528	
Asp	Leu	Lys	Ala	Asn	Ala	Glu	Tyr	Ile	Lys	Met	Ala	Asp	His	Tyr	Val		
				165				170						175			
cca	gtg	cct	gga	gga	cca	aac	aac	aac	aac	tat	gca	aat	gtg	gaa	tta	576	
Pro	Val	Pro	Gly	Gly	Pro	Asn	Asn	Asn	Asn	Tyr	Ala	Asn	Val	Glu	Leu		
			180				185						190				
att	ctt	gat	att	gct	aaa	agg	atc	cca	gtg	cag	gca	gtg	tgg	gct	ggc	624	
Ile	Leu	Asp	Ile	Ala	Lys	Arg	Ile	Pro	Val	Gln	Ala	Val	Trp	Ala	Gly		
		195				200						205					
tgg	ggt	cat	gct	tct	gag	aat	ccc	aaa	cta	ccg	gaa	ctt	ctc	ttg	aaa	672	
Trp	Gly	His	Ala	Ser	Glu	Asn	Pro	Lys	Leu	Pro	Glu	Leu	Leu	Leu	Lys		
	210					215					220						
aat	ggc	att	gcc	ttc	atg	ggt	cct	cca	agc	cag	gcc	atg	tgg	gct	tta	720	
Asn	Gly	Ile	Ala	Phe	Met	Gly	Pro	Pro	Ser	Gln	Ala	Met	Trp	Ala	Leu		
225					230					235				240			
ggg	gat	aag	att	gca	tct	tcc	ata	gtg	gct	caa	act	gca	ggt	atc	cca	768	
Gly	Asp	Lys	Ile	Ala	Ser	Ser	Ile	Val	Ala	Gln	Thr	Ala	Gly	Ile	Pro		
				245				250						255			
act	ctt	ccc	tgg	agc	ggc	agt	ggt	ctt	cgt	gtg	gac	tgg	cag	gaa	aat	816	
Thr	Leu	Pro	Trp	Ser	Gly	Ser	Gly	Leu	Arg	Val	Asp	Trp	Gln	Glu	Asn		
			260					265					270				
gat	ttt	tca	aaa	cgt	atc	tta	aat	gtt	ccc	cag	gag	cta	tat	gaa	aaa	864	
Asp	Phe	Ser	Lys	Arg	Ile	Leu	Asn	Val	Pro	Gln	Glu	Leu	Tyr	Glu	Lys		
			275				280					285					
ggt	tat	gtg	aaa	gat	gtg	gat	gat	ggg	cta	aag	gca	gct	gag	gaa	gtt	912	
Gly	Tyr	Val	Lys	Asp	Val	Asp	Asp	Gly	Leu	Lys	Ala	Ala	Glu	Glu	Val		

290	295	300	
gga tat cca gta atg atc aag gcc tca gag gga gga gga ggg aag gga Gly Tyr Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Lys Gly 305 310 315 320			960
att aga aaa gtc aac aat gca gat gac ttc cct aat ctc ttc aga cag Ile Arg Lys Val Asn Asn Ala Asp Asp Phe Pro Asn Leu Phe Arg Gln 325 330 335			1008
gtt caa gct gaa gtt cct gga tct ccc ata ttt gtg atg aga cta gcc Val Gln Ala Glu Val Pro Gly Ser Pro Ile Phe Val Met Arg Leu Ala 340 345 350			1056
aaa caa tct cgt cat ctg gag gtg cag atc tta gcg gac caa tat ggc Lys Gln Ser Arg His Leu Glu Val Gln Ile Leu Ala Asp Gln Tyr Gly 355 360 365			1104
aat gct atc tct ttg ttt ggt cgt gat tgc tct gta caa cgc agg cat Asn Ala Ile Ser Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His 370 375 380			1152
cag aag att att gaa gaa gca cct gct act att gct act cca gca gta Gln Lys Ile Ile Glu Glu Ala Pro Ala Thr Ile Ala Thr Pro Ala Val 385 390 395 400			1200
ttt gaa cac atg gaa cag tgt gcg gtg aaa ctt gcc aaa atg gtg ggt Phe Glu His Met Glu Gln Cys Ala Val Lys Leu Ala Lys Met Val Gly 405 410 415			1248
tat gtg agt gct ggg act gtg gaa tac ctg tac agc cag gat ggc agc Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp Gly Ser 420 425 430			1296
ttc tac ttt ctg gaa ttg aat cct cgg ctg cag gta gag cac cct tgt Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Cys 435 440 445			1344
aca gag atg gtg gct gat gtc aat ctc cct gca gca cag ctc cag att Thr Glu Met Val Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile 450 455 460			1392
gcc atg ggg att cct cta tat aga atc aag gat atc cgt atg atg tat Ala Met Gly Ile Pro Leu Tyr Arg Ile Lys Asp Ile Arg Met Met Tyr 465 470 475 480			1440
ggg gta tct ccc tgg ggt gat tct ccc att gat ttt gaa gat tct gca Gly Val Ser Pro Trp Gly Asp Ser Pro Ile Asp Phe Glu Asp Ser Ala 485 490 495			1488
cac gtt cct tgt cca agg ggc cat gtt att gct gct cgg atc act agt His Val Pro Cys Pro Arg Gly His Val Ile Ala Ala Arg Ile Thr Ser 500 505 510			1536
gaa aat cca gat gag ggt ttt aag ccc agc tca gga aca gtt cag gag Glu Asn Pro Asp Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu 515 520 525			1584
cta aat ttc cgc agc aat aag aat gtt tgg gga tat ttc agt gtt gct Leu Asn Phe Arg Ser Asn Lys Asn Val Trp Gly Tyr Phe Ser Val Ala 530 535 540			1632

gct gca ggg gga ctt cat gaa ttt gct gat tct cag ttt ggt cac tgc 1680  
 Ala Ala Gly Gly Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys  
 545 550 555 560

ttt tct tgg gga gaa aac aga gaa gag gca att tca aac atg gtg gtg 1728  
 Phe Ser Trp Gly Glu Asn Arg Glu Glu Ala Ile Ser Asn Met Val Val  
 565 570 575

gct ttg aag gag ctg tct att cgg ggt gac ttt cga act aca gtt gaa 1776  
 Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu  
 580 585 590

tac ctg atc aaa ttg tta gag act gaa agc ttt cag atg aac aga att 1824  
 Tyr Leu Ile Lys Leu Leu Glu Thr Glu Ser Phe Gln Met Asn Arg Ile  
 595 600 605

gat act ggc tgg ctg gac aga ctg ata gca gaa aaa gta cag gct gag 1872  
 Asp Thr Gly Trp Leu Asp Arg Leu Ile Ala Glu Lys Val Gln Ala Glu  
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cga cct gac acc atg ttg ggg gtt 1896  
 Arg Pro Asp Thr Met Leu Gly Val  
 625 630

<210> 10  
 <211> 632  
 <212> PRT  
 <213> Homo sapiens

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Met Asp Glu Pro Ser Pro Leu Ala Gln Pro Leu Glu Leu Asn Gln His  
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Ser Arg Phe Ile Ile Gly Ser Val Ser Glu Asp Asn Ser Glu Asp Glu  
 20 25 30

Ile Ser Asn Leu Val Lys Leu Asp Leu Leu Glu Glu Lys Glu Gly Ser  
 35 40 45

Leu Ser Pro Ala Ser Val Gly Ser Asp Thr Leu Ser Asp Leu Gly Ile  
 50 55 60

Ser Ser Leu Gln Asp Gly Leu Ala Leu His Ile Arg Ser Ser Met Ser  
 65 70 75 80

Gly Leu His Leu Val Lys Gln Gly Arg Asp Arg Lys Lys Ile Asp Ser  
 85 90 95

Gln Arg Asp Phe Thr Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe  
 100 105 110



Gly Gly Asn Lys Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile  
 115 120 125

Ala Ala Val Lys Cys Met Arg Ser Ile Arg Arg Trp Ser Tyr Glu Met  
 130 135 140

Phe Arg Asn Glu Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu  
 145 150 155 160

Asp Leu Lys Ala Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val  
 165 170 175

Pro Val Pro Gly Gly Pro Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu  
 180 185 190

Ile Leu Asp Ile Ala Lys Arg Ile Pro Val Gln Ala Val Trp Ala Gly  
 195 200 205

Trp Gly His Ala Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Leu Lys  
 210 215 220

Asn Gly Ile Ala Phe Met Gly Pro Pro Ser Gln Ala Met Trp Ala Leu  
 225 230 235 240

Gly Asp Lys Ile Ala Ser Ser Ile Val Ala Gln Thr Ala Gly Ile Pro  
 245 250 255

Thr Leu Pro Trp Ser Gly Ser Gly Leu Arg Val Asp Trp Gln Glu Asn  
 260 265 270

Asp Phe Ser Lys Arg Ile Leu Asn Val Pro Gln Glu Leu Tyr Glu Lys  
 275 280 285

Gly Tyr Val Lys Asp Val Asp Asp Gly Leu Lys Ala Ala Glu Glu Val  
 290 295 300

Gly Tyr Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly  
 305 310 315 320

Ile Arg Lys Val Asn Asn Ala Asp Asp Phe Pro Asn Leu Phe Arg Gln  
 325 330 335

Val Gln Ala Glu Val Pro Gly Ser Pro Ile Phe Val Met Arg Leu Ala  
 340 345 350

Lys Gln Ser Arg His Leu Glu Val Gln Ile Leu Ala Asp Gln Tyr Gly

355	360	365
Asn Ala Ile Ser Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His		
370	375	380
Gln Lys Ile Ile Glu Glu Ala Pro Ala Thr Ile Ala Thr Pro Ala Val		
385	390	395
Phe Glu His Met Glu Gln Cys Ala Val Lys Leu Ala Lys Met Val Gly		
405	410	415
Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp Gly Ser		
420	425	430
Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Cys		
435	440	445
Thr Glu Met Val Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile		
450	455	460
Ala Met Gly Ile Pro Leu Tyr Arg Ile Lys Asp Ile Arg Met Met Tyr		
465	470	475
Gly Val Ser Pro Trp Gly Asp Ser Pro Ile Asp Phe Glu Asp Ser Ala		
485	490	495
His Val Pro Cys Pro Arg Gly His Val Ile Ala Ala Arg Ile Thr Ser		
500	505	510
Glu Asn Pro Asp Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu		
515	520	525
Leu Asn Phe Arg Ser Asn Lys Asn Val Trp Gly Tyr Phe Ser Val Ala		
530	535	540
Ala Ala Gly Gly Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys		
545	550	555
Phe Ser Trp Gly Glu Asn Arg Glu Glu Ala Ile Ser Asn Met Val Val		
565	570	575
Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu		
580	585	590
Tyr Leu Ile Lys Leu Leu Glu Thr Glu Ser Phe Gln Met Asn Arg Ile		
595	600	605

Asp Thr Gly Trp Leu Asp Arg Leu Ile Ala Glu Lys Val Gln Ala Glu  
610 615 620

Arg Pro Asp Thr Met Leu Gly Val  
625 630

<210> 11  
<211> 2322  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (1)..(2322)  
<223> Human ACCase2 (beta) BC domain (aa 1-774)

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Met Val Leu Leu Leu Cys Leu Ser Cys Leu Ile Phe Ser Cys Leu Thr  
1 5 10 15  
  
ttt tcc tgg tta aaa atc tgg ggg aaa atg acg gac tcc aag ccg atc 96  
Phe Ser Trp Leu Lys Ile Trp Gly Lys Met Thr Asp Ser Lys Pro Ile  
20 25 30  
  
acc aag agt aaa tca gaa gca aac ctc atc ccg agc cag gag ccc ttt 144  
Thr Lys Ser Lys Ser Glu Ala Asn Leu Ile Pro Ser Gln Glu Pro Phe  
35 40 45  
  
cca gcc tct gat aac tca ggg gag aca ccg cag aga aat ggg gag ggc 192  
Pro Ala Ser Asp Asn Ser Gly Glu Thr Pro Gln Arg Asn Gly Glu Gly  
50 55 60  
  
cac act ctg ccc aag aca ccc agc cag gcc gag cca gcc tcc cac aaa 240  
His Thr Leu Pro Lys Thr Pro Ser Gln Ala Glu Pro Ala Ser His Lys  
65 70 75 80  
  
ggc ccc aaa gat gcc ggt cgg cgg aga aac tcc cta cca ccc tcc cac 288  
Gly Pro Lys Asp Ala Gly Arg Arg Arg Asn Ser Leu Pro Pro Ser His  
85 90 95  
  
cag aag ccc cca aga aac ccc ctt tct tcc agt gac gca gca ccc tcc 336  
Gln Lys Pro Pro Arg Asn Pro Leu Ser Ser Ser Asp Ala Ala Pro Ser  
100 105 110  
  
cca gag ctt caa gcc aac ggg act ggg aca caa ggt ctg gag gcc aca 384  
Pro Glu Leu Gln Ala Asn Gly Thr Gly Thr Gln Gly Leu Glu Ala Thr  
115 120 125  
  
gat acc aat ggc ctg tcc tcc tca gcc agg ccc cag ggc cag caa gct 432  
Asp Thr Asn Gly Leu Ser Ser Ser Ala Arg Pro Gln Gly Gln Gln Ala  
130 135 140  
  
ggc tcc ccc tcc aaa gaa gac aag aag cag gca aac atc aag agg cag 480  
Gly Ser Pro Ser Lys Glu Asp Lys Lys Gln Ala Asn Ile Lys Arg Gln  
145 150 155 160

ctg atg acc aac ttc atc ctg ggc tct ttt gat gac tac tcc tct gac	528
Leu Met Thr Asn Phe Ile Leu Gly Ser Phe Asp Asp Tyr Ser Ser Asp	
165 170 175	
gag gac tct gtt gct ggc tca tct cgt gag tct acc cgg aag ggc agc	576
Glu Asp Ser Val Ala Gly Ser Ser Arg Glu Ser Thr Arg Lys Gly Ser	
180 185 190	
cgg gcc agc ttg ggg gcc ctg tcc ctg gag gct tat ctg acc aca ggt	624
Arg Ala Ser Leu Gly Ala Leu Ser Leu Glu Ala Tyr Leu Thr Thr Gly	
195 200 205	
gaa gct gag acc cgc gtc ccc act atg agg ccg agc atg tcg gga ctc	672
Glu Ala Glu Thr Arg Val Pro Thr Met Arg Pro Ser Met Ser Gly Leu	
210 215 220	
cac ctg gtg aag agg gga cgg gaa cac aag aag ctg gac ctg cac aga	720
His Leu Val Lys Arg Gly Arg Glu His Lys Lys Leu Asp Leu His Arg	
225 230 235 240	
gac ttt acc gtg gct tct ccc gct gag ttt gtc aca cgc ttt ggg ggg	768
Asp Phe Thr Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe Gly Gly	
245 250 255	
gat cgg gtc atc gag aag gtg ctt att gcc aac aac ggg att gcc gcc	816
Asp Arg Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile Ala Ala	
260 265 270	
gtg aag tgc atg cgc tcc atc cgc agg tgg gcc tat gag atg ttc cgc	864
Val Lys Cys Met Arg Ser Ile Arg Arg Trp Ala Tyr Glu Met Phe Arg	
275 280 285	
aac gag cgg gcc atc cgg ttt gtt gtg atg gtg acc ccc gag gac ctt	912
Asn Glu Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu Asp Leu	
290 295 300	
aag gcc aac gca gag tac atc aag atg gcg gat cat tac gtc ccc gtc	960
Lys Ala Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val Pro Val	
305 310 315 320	
cca gga ggg ccc aat aac aac aac tat gcc aac gtg gag ctg att gtg	1008
Pro Gly Gly Pro Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Val	
325 330 335	
gac att gcc aag aga att cct ttg cag gcg gtg tgg gct ggc tgg ggc	1056
Asp Ile Ala Lys Arg Ile Pro Leu Gln Ala Val Trp Ala Gly Trp Gly	
340 345 350	
cat gct tca gaa aac cct aaa ctt ccg gag ctg ctg tgc aag aat gga	1104
His Ala Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Cys Lys Asn Gly	
355 360 365	
gtt gct ttc tta ggc cct ccc agt gag gcc atg tgg gcc tta gga gat	1152
Val Ala Phe Leu Gly Pro Pro Ser Glu Ala Met Trp Ala Leu Gly Asp	
370 375 380	
aag atc gcc tcc acc gtt gtc gcc cag acg cta cag gtc cca acc ctg	1200
Lys Ile Ala Ser Thr Val Val Ala Gln Thr Leu Gln Val Pro Thr Leu	
385 390 395 400	

ccc agg agt gga agc ggc ctg aca gtg gag tgg aca gaa gat gat ctg	1248
Pro Arg Ser Gly Ser Gly Leu Thr Val Glu Trp Thr Glu Asp Asp Leu	
405 410 415	
cag cag gga aaa aga atc agt gtc cca gaa gat gtt tat gac aag ggt	1296
Gln Gln Gly Lys Arg Ile Ser Val Pro Glu Asp Val Tyr Asp Lys Gly	
420 425 430	
tgc gtg aaa gac gta gat gag ggc ttg gag gca gca gaa aga att ggt	1344
Cys Val Lys Asp Val Asp Glu Gly Leu Glu Ala Ala Glu Arg Ile Gly	
435 440 445	
ttt cca ttg atg atc aaa gct tct gaa ggt ggc gga ggg aag gga atc	1392
Phe Pro Leu Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile	
450 455 460	
cgg aag gct gag agt gcg gag gac ttc ccg atc ctt ttc aga caa gta	1440
Arg Lys Ala Glu Ser Ala Glu Asp Phe Pro Ile Leu Phe Arg Gln Val	
465 470 475 480	
cag agt gag atc cca ggc tcg ccc atc ttt ctc atg aag ctg gcc cag	1488
Gln Ser Glu Ile Pro Gly Ser Pro Ile Phe Leu Met Lys Leu Ala Gln	
485 490 495	
cac gcc cgt cac ctg gaa gtt cag atc ctc gct gac cag tat ggg aat	1536
His Ala Arg His Leu Glu Val Gln Ile Leu Ala Asp Gln Tyr Gly Asn	
500 505 510	
gct gtg tct ctg ttt ggt cgc gac tgc tcc atc cag cgg cgg cat cag	1584
Ala Val Ser Leu Phe Gly Arg Asp Cys Ser Ile Gln Arg Arg His Gln	
515 520 525	
aag atc gtt gag gaa gca ccg gcc acc atc gcc ccg ctg gcc ata ttc	1632
Lys Ile Val Glu Glu Ala Pro Ala Thr Ile Ala Pro Leu Ala Ile Phe	
530 535 540	
gag ttc atg gag cag tgt gcc atc cgc ctg gcc aag acc gtg ggc tat	1680
Glu Phe Met Glu Gln Cys Ala Ile Arg Leu Ala Lys Thr Val Gly Tyr	
545 550 555 560	
gtg agt gca ggg aca gtg gaa tac ctc tat agt cag gat ggc agc ttc	1728
Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp Gly Ser Phe	
565 570 575	
cac ttc ttg gag ctg aat cct cgc ttg cag gtg gaa cat ccc tgc aca	1776
His Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Cys Thr	
580 585 590	
gaa atg att gct gat gtt aat ctg ccg gcc gcc cag cta cag atc gcc	1824
Glu Met Ile Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala	
595 600 605	
atg ggc gtg cca ctg cac cgg ctg aag gat atc cgg ctt ctg tat gga	1872
Met Gly Val Pro Leu His Arg Leu Lys Asp Ile Arg Leu Leu Tyr Gly	
610 615 620	
gag tca cca tgg gga gtg act ccc att tct ttt gaa acc ccc tca aac	1920
Glu Ser Pro Trp Gly Val Thr Pro Ile Ser Phe Glu Thr Pro Ser Asn	
625 630 635 640	
cct ccc ctc gcc cga ggc cac gtc att gcc gcc aga atc acc agc gaa	1968

Pro	Pro	Leu	Ala	Arg	Gly	His	Val	Ile	Ala	Ala	Arg	Ile	Thr	Ser	Glu		
				645					650					655			
aac	cca	gac	gag	ggt	ttt	aag	ccg	agc	tcc	ggg	act	gtc	cag	gaa	ctg		2016
Asn	Pro	Asp	Glu	Gly	Phe	Lys	Pro	Ser	Ser	Gly	Thr	Val	Gln	Glu	Leu		
			660					665					670				
aat	ttc	cgg	agc	agc	aag	aac	gtg	tgg	ggg	tac	ttc	agc	gtg	gcc	gct		2064
Asn	Phe	Arg	Ser	Ser	Lys	Asn	Val	Trp	Gly	Tyr	Phe	Ser	Val	Ala	Ala		
		675					680					685					
act	gga	ggc	ctg	cac	gag	ttt	gcg	gat	tcc	caa	ttt	ggg	cac	tgc	ttc		2112
Thr	Gly	Gly	Leu	His	Glu	Phe	Ala	Asp	Ser	Gln	Phe	Gly	His	Cys	Phe		
	690					695					700						
tcc	tgg	gga	gag	aac	cgg	aaa	gag	gcc	att	tcg	aac	atg	gtg	gtg	gct		2160
Ser	Trp	Gly	Glu	Asn	Arg	Lys	Glu	Ala	Ile	Ser	Asn	Met	Val	Val	Ala		
705					710					715				720			
ttg	aag	gaa	ctg	tcc	atc	cga	ggt	gac	ttt	agg	act	acc	gtg	gaa	tac		2208
Leu	Lys	Glu	Leu	Ser	Ile	Arg	Gly	Asp	Phe	Arg	Thr	Thr	Val	Glu	Tyr		
				725					730					735			
ctc	att	aac	ctc	ctg	gag	acc	gag	agc	ttc	cag	aac	aac	gac	atc	gac		2256
Leu	Ile	Asn	Leu	Leu	Glu	Thr	Glu	Ser	Phe	Gln	Asn	Asn	Asp	Ile	Asp		
			740					745					750				
acc	ggg	tgg	ttg	gac	tac	ctc	att	gct	gag	aaa	gtg	cag	gag	aaa	ccg		2304
Thr	Gly	Trp	Leu	Asp	Tyr	Leu	Ile	Ala	Glu	Lys	Val	Gln	Glu	Lys	Pro		
		755					760					765					
gat	atc	atg	ctt	ggg	gtg												2322
Asp	Ile	Met	Leu	Gly	Val												
			770														

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 <211> 774  
 <212> PRT  
 <213> Homo sapiens

<400> 12

Met	Val	Leu	Leu	Leu	Cys	Leu	Ser	Cys	Leu	Ile	Phe	Ser	Cys	Leu	Thr	
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Phe	Ser	Trp	Leu	Lys	Ile	Trp	Gly	Lys	Met	Thr	Asp	Ser	Lys	Pro	Ile	
			20					25					30			

Thr	Lys	Ser	Lys	Ser	Glu	Ala	Asn	Leu	Ile	Pro	Ser	Gln	Glu	Pro	Phe	
		35					40					45				

Pro	Ala	Ser	Asp	Asn	Ser	Gly	Glu	Thr	Pro	Gln	Arg	Asn	Gly	Glu	Gly	
	50					55					60					

His	Thr	Leu	Pro	Lys	Thr	Pro	Ser	Gln	Ala	Glu	Pro	Ala	Ser	His	Lys	
65					70					75					80	

Gly Pro Lys Asp Ala Gly Arg Arg Arg Asn Ser Leu Pro Pro Ser His  
 85 90 95

Gln Lys Pro Pro Arg Asn Pro Leu Ser Ser Ser Asp Ala Ala Pro Ser  
 100 105 110

Pro Glu Leu Gln Ala Asn Gly Thr Gly Thr Gln Gly Leu Glu Ala Thr  
 115 120 125

Asp Thr Asn Gly Leu Ser Ser Ser Ala Arg Pro Gln Gly Gln Gln Ala  
 130 135 140

Gly Ser Pro Ser Lys Glu Asp Lys Lys Gln Ala Asn Ile Lys Arg Gln  
 145 150 155 160

Leu Met Thr Asn Phe Ile Leu Gly Ser Phe Asp Asp Tyr Ser Ser Asp  
 165 170 175

Glu Asp Ser Val Ala Gly Ser Ser Arg Glu Ser Thr Arg Lys Gly Ser  
 180 185 190

Arg Ala Ser Leu Gly Ala Leu Ser Leu Glu Ala Tyr Leu Thr Thr Gly  
 195 200 205

Glu Ala Glu Thr Arg Val Pro Thr Met Arg Pro Ser Met Ser Gly Leu  
 210 215 220

His Leu Val Lys Arg Gly Arg Glu His Lys Lys Leu Asp Leu His Arg  
 225 230 235 240

Asp Phe Thr Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe Gly Gly  
 245 250 255

Asp Arg Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile Ala Ala  
 260 265 270

Val Lys Cys Met Arg Ser Ile Arg Arg Trp Ala Tyr Glu Met Phe Arg  
 275 280 285

Asn Glu Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu Asp Leu  
 290 295 300

Lys Ala Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val Pro Val  
 305 310 315 320

Pro Gly Gly Pro Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Val  
 325 330 335

Asp Ile Ala Lys Arg Ile Pro Leu Gln Ala Val Trp Ala Gly Trp Gly  
 340 345 350

His Ala Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Cys Lys Asn Gly  
 355 360 365

Val Ala Phe Leu Gly Pro Pro Ser Glu Ala Met Trp Ala Leu Gly Asp  
 370 375 380

Lys Ile Ala Ser Thr Val Val Ala Gln Thr Leu Gln Val Pro Thr Leu  
 385 390 395 400

Pro Arg Ser Gly Ser Gly Leu Thr Val Glu Trp Thr Glu Asp Asp Leu  
 405 410 415

Gln Gln Gly Lys Arg Ile Ser Val Pro Glu Asp Val Tyr Asp Lys Gly  
 420 425 430

Cys Val Lys Asp Val Asp Glu Gly Leu Glu Ala Ala Glu Arg Ile Gly  
 435 440 445

Phe Pro Leu Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile  
 450 455 460

Arg Lys Ala Glu Ser Ala Glu Asp Phe Pro Ile Leu Phe Arg Gln Val  
 465 470 475 480

Gln Ser Glu Ile Pro Gly Ser Pro Ile Phe Leu Met Lys Leu Ala Gln  
 485 490 495

His Ala Arg His Leu Glu Val Gln Ile Leu Ala Asp Gln Tyr Gly Asn  
 500 505 510

Ala Val Ser Leu Phe Gly Arg Asp Cys Ser Ile Gln Arg Arg His Gln  
 515 520 525

Lys Ile Val Glu Glu Ala Pro Ala Thr Ile Ala Pro Leu Ala Ile Phe  
 530 535 540

Glu Phe Met Glu Gln Cys Ala Ile Arg Leu Ala Lys Thr Val Gly Tyr  
 545 550 555 560



Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp Gly Ser Phe  
565 570 575

His Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Cys Thr  
580 585 590

Glu Met Ile Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala  
595 600 605

Met Gly Val Pro Leu His Arg Leu Lys Asp Ile Arg Leu Leu Tyr Gly  
610 615 620

Glu Ser Pro Trp Gly Val Thr Pro Ile Ser Phe Glu Thr Pro Ser Asn  
625 630 635 640

Pro Pro Leu Ala Arg Gly His Val Ile Ala Ala Arg Ile Thr Ser Glu  
645 650 655

Asn Pro Asp Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu Leu  
660 665 670

Asn Phe Arg Ser Ser Lys Asn Val Trp Gly Tyr Phe Ser Val Ala Ala  
675 680 685

Thr Gly Gly Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys Phe  
690 695 700

Ser Trp Gly Glu Asn Arg Lys Glu Ala Ile Ser Asn Met Val Val Ala  
705 710 715 720

Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr  
725 730 735

Leu Ile Asn Leu Leu Glu Thr Glu Ser Phe Gln Asn Asn Asp Ile Asp  
740 745 750

Thr Gly Trp Leu Asp Tyr Leu Ile Ala Glu Lys Val Gln Glu Lys Pro  
755 760 765

Asp Ile Met Leu Gly Val  
770

<210> 13  
<211> 1596  
<212> DNA  
<213> Homo sapiens

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<220>
<221> CDS
<222> (1) .. (1596)
<223> N-terminal deleted Human ACCase1 BC domain (AAs 102-632)

<400> 13
atg gtg gct tct cca gca gaa ttt gtt act cgc ttt ggg gga aat aaa      48
Met Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe Gly Gly Asn Lys
1          5          10          15

gtg att gag aag gtt ctt att gct aac aat ggc att gca gca gtg aaa      96
Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys
          20          25          30

tgc atg cgg tct atc cgt agg tgg tct tat gaa atg ttt cga aat gaa      144
Cys Met Arg Ser Ile Arg Arg Trp Ser Tyr Glu Met Phe Arg Asn Glu
          35          40          45

cgt gca att aga ttc gtt gtc atg gtc aca cct gaa gac ctt aaa gcc      192
Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu Asp Leu Lys Ala
          50          55          60

aat gca gaa tac att aag atg gca gat cac tat gtg cca gtg cct gga      240
Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val Pro Val Pro Gly
65          70          75          80

gga cca aac aac aac aac tat gca aat gtg gaa tta att ctt gat att      288
Gly Pro Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Leu Asp Ile
          85          90          95

gct aaa agg atc cca gtg cag gca gtg tgg gct ggc tgg ggt cat gct      336
Ala Lys Arg Ile Pro Val Gln Ala Val Trp Ala Gly Trp Gly His Ala
          100          105          110

tct gag aat ccc aaa cta ccg gaa ctt ctc ttg aaa aat ggc att gcc      384
Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Leu Lys Asn Gly Ile Ala
          115          120          125

ttc atg ggt cct cca agc cag gcc atg tgg gct tta ggg gat aag att      432
Phe Met Gly Pro Pro Ser Gln Ala Met Trp Ala Leu Gly Asp Lys Ile
          130          135          140

gca tct tcc ata gtg gct caa act gca ggt atc cca act ctt ccc tgg      480
Ala Ser Ser Ile Val Ala Gln Thr Ala Gly Ile Pro Thr Leu Pro Trp
145          150          155          160

agc ggc agt ggt ctt cgt gtg gac tgg cag gaa aat gat ttt tca aaa      528
Ser Gly Ser Gly Leu Arg Val Asp Trp Gln Glu Asn Asp Phe Ser Lys
          165          170          175

cgt atc tta aat gtt ccc cag gag cta tat gaa aaa ggt tat gtg aaa      576
Arg Ile Leu Asn Val Pro Gln Glu Leu Tyr Glu Lys Gly Tyr Val Lys
          180          185          190

gat gtg gat gat ggg cta aag gca gct gag gaa gtt gga tat cca gta      624
Asp Val Asp Asp Gly Leu Lys Ala Ala Glu Glu Val Gly Tyr Pro Val
          195          200          205

atg atc aag gcc tca gag gga gga gga ggg aag gga att aga aaa gtc      672
Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Lys Val

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210	215	220	
aac aat gca gat gac ttc cct aat ctc ttc aga cag gtt caa gct gaa Asn Asn Ala Asp Asp Phe Pro Asn Leu Phe Arg Gln Val Gln Ala Glu 225 230 235 240			720
ggt cct gga tct ccc ata ttt gtg atg aga cta gcc aaa caa tct cgt Val Pro Gly Ser Pro Ile Phe Val Met Arg Leu Ala Lys Gln Ser Arg 245 250 255			768
cat ctg gag gtg cag atc tta gcg gac caa tat ggc aat gct atc tct His Leu Glu Val Gln Ile Leu Ala Asp Gln Tyr Gly Asn Ala Ile Ser 260 265 270			816
ttg ttt ggt cgt gat tgc tct gta caa cgc agg cat cag aag att att Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile Ile 275 280 285			864
gaa gaa gca cct gct act att gct act cca gca gta ttt gaa cac atg Glu Glu Ala Pro Ala Thr Ile Ala Thr Pro Ala Val Phe Glu His Met 290 295 300			912
gaa cag tgt gcg gtg aaa ctt gcc aaa atg gtg ggt tat gtg agt gct Glu Gln Cys Ala Val Lys Leu Ala Lys Met Val Gly Tyr Val Ser Ala 305 310 315 320			960
ggg act gtg gaa tac ctg tac agc cag gat ggc agc ttc tac ttt ctg Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp Gly Ser Phe Tyr Phe Leu 325 330 335			1008
gaa ttg aat cct cgg ctg cag gta gag cac cct tgt aca gag atg gtg Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Cys Thr Glu Met Val 340 345 350			1056
gct gat gtc aat ctc cct gca gca cag ctc cag att gcc atg ggg att Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala Met Gly Ile 355 360 365			1104
cct cta tat aga atc aag gat atc cgt atg atg tat ggg gta tct ccc Pro Leu Tyr Arg Ile Lys Asp Ile Arg Met Met Tyr Gly Val Ser Pro 370 375 380			1152
tgg ggt gat tct ccc att gat ttt gaa gat tct gca cac gtt cct tgt Trp Gly Asp Ser Pro Ile Asp Phe Glu Asp Ser Ala His Val Pro Cys 385 390 395 400			1200
cca agg ggc cat gtt att gct gct cgg atc act agt gaa aat cca gat Pro Arg Gly His Val Ile Ala Ala Arg Ile Thr Ser Glu Asn Pro Asp 405 410 415			1248
gag ggt ttt aag ccc agc tca gga aca gtt cag gag cta aat ttc cgc Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu Leu Asn Phe Arg 420 425 430			1296
agc aat aag aat gtt tgg gga tat ttc agt gtt gct gct gca ggg gga Ser Asn Lys Asn Val Trp Gly Tyr Phe Ser Val Ala Ala Ala Gly Gly 435 440 445			1344
ctt cat gaa ttt gct gat tct cag ttt ggt cac tgc ttt tct tgg gga Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys Phe Ser Trp Gly 450 455 460			1392

gaa aac aga gaa gag gca att tca aac atg gtg gtg gct ttg aag gag 1440  
 Glu Asn Arg Glu Glu Ala Ile Ser Asn Met Val Val Ala Leu Lys Glu  
 465 470 475 480

ctg tct att cgg ggt gac ttt cga act aca gtt gaa tac ctg atc aaa 1488  
 Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys  
 485 490 495

ttg tta gag act gaa agc ttt cag atg aac aga att gat act ggc tgg 1536  
 Leu Leu Glu Thr Glu Ser Phe Gln Met Asn Arg Ile Asp Thr Gly Trp  
 500 505 510

ctg gac aga ctg ata gca gaa aaa gta cag gct gag cga cct gac acc 1584  
 Leu Asp Arg Leu Ile Ala Glu Lys Val Gln Ala Glu Arg Pro Asp Thr  
 515 520 525

atg ttg ggg gtt 1596  
 Met Leu Gly Val  
 530

<210> 14  
 <211> 532  
 <212> PRT  
 <213> Homo sapiens

<400> 14

Met Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe Gly Gly Asn Lys  
 1 5 10 15

Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys  
 20 25 30

Cys Met Arg Ser Ile Arg Arg Trp Ser Tyr Glu Met Phe Arg Asn Glu  
 35 40 45

Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu Asp Leu Lys Ala  
 50 55 60

Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val Pro Val Pro Gly  
 65 70 75 80

Gly Pro Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Leu Asp Ile  
 85 90 95

Ala Lys Arg Ile Pro Val Gln Ala Val Trp Ala Gly Trp Gly His Ala  
 100 105 110

Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Leu Lys Asn Gly Ile Ala  
 115 120 125

Phe Met Gly Pro Pro Ser Gln Ala Met Trp Ala Leu Gly Asp Lys Ile  
 130 135 140

Ala Ser Ser Ile Val Ala Gln Thr Ala Gly Ile Pro Thr Leu Pro Trp  
 145 150 155 160

Ser Gly Ser Gly Leu Arg Val Asp Trp Gln Glu Asn Asp Phe Ser Lys  
 165 170 175

Arg Ile Leu Asn Val Pro Gln Glu Leu Tyr Glu Lys Gly Tyr Val Lys  
 180 185 190

Asp Val Asp Asp Gly Leu Lys Ala Ala Glu Glu Val Gly Tyr Pro Val  
 195 200 205

Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Lys Val  
 210 215 220

Asn Asn Ala Asp Asp Phe Pro Asn Leu Phe Arg Gln Val Gln Ala Glu  
 225 230 235 240

Val Pro Gly Ser Pro Ile Phe Val Met Arg Leu Ala Lys Gln Ser Arg  
 245 250 255

His Leu Glu Val Gln Ile Leu Ala Asp Gln Tyr Gly Asn Ala Ile Ser  
 260 265 270

Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile Ile  
 275 280 285

Glu Glu Ala Pro Ala Thr Ile Ala Thr Pro Ala Val Phe Glu His Met  
 290 295 300

Glu Gln Cys Ala Val Lys Leu Ala Lys Met Val Gly Tyr Val Ser Ala  
 305 310 315 320

Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp Gly Ser Phe Tyr Phe Leu  
 325 330 335

Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Cys Thr Glu Met Val  
 340 345 350

Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala Met Gly Ile  
 355 360 365

Pro Leu Tyr Arg Ile Lys Asp Ile Arg Met Met Tyr Gly Val Ser Pro

370                                      375                                      380  
 Trp Gly Asp Ser Pro Ile Asp Phe Glu Asp Ser Ala His Val Pro Cys  
 385                                      390                                      395                                      400  
 Pro Arg Gly His Val Ile Ala Ala Arg Ile Thr Ser Glu Asn Pro Asp  
                                     405                                      410                                      415  
 Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu Leu Asn Phe Arg  
                                     420                                      425                                      430  
 Ser Asn Lys Asn Val Trp Gly Tyr Phe Ser Val Ala Ala Ala Gly Gly  
                                     435                                      440                                      445  
 Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys Phe Ser Trp Gly  
                                     450                                      455                                      460  
 Glu Asn Arg Glu Glu Ala Ile Ser Asn Met Val Val Ala Leu Lys Glu  
 465                                      470                                      475                                      480  
 Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys  
                                     485                                      490                                      495  
 Leu Leu Glu Thr Glu Ser Phe Gln Met Asn Arg Ile Asp Thr Gly Trp  
                                     500                                      505                                      510  
 Leu Asp Arg Leu Ile Ala Glu Lys Val Gln Ala Glu Arg Pro Asp Thr  
                                     515                                      520                                      525  
 Met Leu Gly Val  
                                     530

<210> 15  
 <211> 1596  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(1596)  
 <223> N-terminal deleted Human ACCase2 BC domain (AAs 244-774)

<400> 15  
 atg gtg gct tct ccc gct gag ttt gtc aca cgc ttt ggg ggg gat cgg                                      48  
 Met Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe Gly Gly Asp Arg  
 1                                      5                                      10                                      15  
 gtc atc gag aag gtg ctt att gcc aac aac ggg att gcc gcc gtg aag                                      96  
 Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys

20					25					30						
tgc	atg	cgc	tcc	atc	cgc	agg	tgg	gcc	tat	gag	atg	ttc	cgc	aac	gag	144
Cys	Met	Arg	Ser	Ile	Arg	Arg	Trp	Ala	Tyr	Glu	Met	Phe	Arg	Asn	Glu	
		35					40					45				
cgg	gcc	atc	cgg	ttt	gtt	gtg	atg	gtg	acc	ccc	gag	gac	ctt	aag	gcc	192
Arg	Ala	Ile	Arg	Phe	Val	Val	Met	Val	Thr	Pro	Glu	Asp	Leu	Lys	Ala	
	50					55					60					
aac	gca	gag	tac	atc	aag	atg	gcg	gat	cat	tac	gtc	ccc	gtc	cca	gga	240
Asn	Ala	Glu	Tyr	Ile	Lys	Met	Ala	Asp	His	Tyr	Val	Pro	Val	Pro	Gly	
65					70					75					80	
ggg	ccc	aat	aac	aac	aac	tat	gcc	aac	gtg	gag	ctg	att	gtg	gac	att	288
Gly	Pro	Asn	Asn	Asn	Asn	Tyr	Ala	Asn	Val	Glu	Leu	Ile	Val	Asp	Ile	
			85						90					95		
gcc	aag	aga	att	cct	ttg	cag	gcg	gtg	tgg	gct	ggc	tgg	ggc	cat	gct	336
Ala	Lys	Arg	Ile	Pro	Leu	Gln	Ala	Val	Trp	Ala	Gly	Trp	Gly	His	Ala	
			100					105					110			
tca	gaa	aac	cct	aaa	ctt	ccg	gag	ctg	ctg	tgc	aag	aat	gga	gtt	gct	384
Ser	Glu	Asn	Pro	Lys	Leu	Pro	Glu	Leu	Leu	Cys	Lys	Asn	Gly	Val	Ala	
		115					120					125				
ttc	tta	ggc	cct	ccc	agt	gag	gcc	atg	tgg	gcc	tta	gga	gat	aag	atc	432
Phe	Leu	Gly	Pro	Pro	Ser	Glu	Ala	Met	Trp	Ala	Leu	Gly	Asp	Lys	Ile	
	130					135					140					
gcc	tcc	acc	gtt	gtc	gcc	cag	acg	cta	cag	gtc	cca	acc	ctg	ccc	agg	480
Ala	Ser	Thr	Val	Val	Ala	Gln	Thr	Leu	Gln	Val	Pro	Thr	Leu	Pro	Arg	
145					150					155					160	
agt	gga	agc	ggc	ctg	aca	gtg	gag	tgg	aca	gaa	gat	gat	ctg	cag	cag	528
Ser	Gly	Ser	Gly	Leu	Thr	Val	Glu	Trp	Thr	Glu	Asp	Asp	Leu	Gln	Gln	
				165				170						175		
gga	aaa	aga	atc	agt	gtc	cca	gaa	gat	gtt	tat	gac	aag	ggg	tgc	gtg	576
Gly	Lys	Arg	Ile	Ser	Val	Pro	Glu	Asp	Val	Tyr	Asp	Lys	Gly	Cys	Val	
			180					185					190			
aaa	gac	gta	gat	gag	ggc	ttg	gag	gca	gca	gaa	aga	att	ggg	ttt	cca	624
Lys	Asp	Val	Asp	Glu	Gly	Leu	Glu	Ala	Ala	Glu	Arg	Ile	Gly	Phe	Pro	
	195					200						205				
ttg	atg	atc	aaa	gct	tct	gaa	ggg	ggc	gga	ggg	aag	gga	atc	cgg	aag	672
Leu	Met	Ile	Lys	Ala	Ser	Glu	Gly	Gly	Gly	Gly	Lys	Gly	Ile	Arg	Lys	
	210					215					220					
gct	gag	agt	gcg	gag	gac	ttc	ccg	atc	ctt	ttc	aga	caa	gta	cag	agt	720
Ala	Glu	Ser	Ala	Glu	Asp	Phe	Pro	Ile	Leu	Phe	Arg	Gln	Val	Gln	Ser	
225					230					235					240	
gag	atc	cca	ggc	tcg	ccc	atc	ttt	ctc	atg	aag	ctg	gcc	cag	cac	gcc	768
Glu	Ile	Pro	Gly	Ser	Pro	Ile	Phe	Leu	Met	Lys	Leu	Ala	Gln	His	Ala	
				245					250					255		
cgt	cac	ctg	gaa	gtt	cag	atc	ctc	gct	gac	cag	tat	ggg	aat	gct	gtg	816
Arg	His	Leu	Glu	Val	Gln	Ile	Leu	Ala	Asp	Gln	Tyr	Gly	Asn	Ala	Val	
			260					265					270			

tct ctg ttt ggt cgc gac tgc tcc atc cag cgg cgg cat cag aag atc	864
Ser Leu Phe Gly Arg Asp Cys Ser Ile Gln Arg Arg His Gln Lys Ile	
275 280 285	
gtt gag gaa gca ccg gcc acc atc gcc ccg ctg gcc ata ttc gag ttc	912
Val Glu Glu Ala Pro Ala Thr Ile Ala Pro Leu Ala Ile Phe Glu Phe	
290 295 300	
atg gag cag tgt gcc atc cgc ctg gcc aag acc gtg ggc tat gtg agt	960
Met Glu Gln Cys Ala Ile Arg Leu Ala Lys Thr Val Gly Tyr Val Ser	
305 310 315 320	
gca ggg aca gtg gaa tac ctc tat agt cag gat ggc agc ttc cac ttc	1008
Ala Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp Gly Ser Phe His Phe	
325 330 335	
ttg gag ctg aat cct cgc ttg cag gtg gaa cat ccc tgc aca gaa atg	1056
Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Cys Thr Glu Met	
340 345 350	
att gct gat gtt aat ctg ccg gcc gcc cag cta cag atc gcc atg ggc	1104
Ile Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala Met Gly	
355 360 365	
gtg cca ctg cac cgg ctg aag gat atc cgg ctt ctg tat gga gag tca	1152
Val Pro Leu His Arg Leu Lys Asp Ile Arg Leu Leu Tyr Gly Glu Ser	
370 375 380	
cca tgg gga gtg act ccc att tct ttt gaa acc ccc tca aac cct ccc	1200
Pro Trp Gly Val Thr Pro Ile Ser Phe Glu Thr Pro Ser Asn Pro Pro	
385 390 395 400	
ctc gcc cga ggc cac gtc att gcc gcc aga atc acc agc gaa aac cca	1248
Leu Ala Arg Gly His Val Ile Ala Ala Arg Ile Thr Ser Glu Asn Pro	
405 410 415	
gac gag ggt ttt aag ccg agc tcc ggg act gtc cag gaa ctg aat ttc	1296
Asp Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu Leu Asn Phe	
420 425 430	
cgg agc agc aag aac gtg tgg ggt tac ttc agc gtg gcc gct act gga	1344
Arg Ser Ser Lys Asn Val Trp Gly Tyr Phe Ser Val Ala Ala Thr Gly	
435 440 445	
ggc ctg cac gag ttt gcg gat tcc caa ttt ggg cac tgc ttc tcc tgg	1392
Gly Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys Phe Ser Trp	
450 455 460	
gga gag aac cgg aaa gag gcc att tcg aac atg gtg gtg gct ttg aag	1440
Gly Glu Asn Arg Lys Glu Ala Ile Ser Asn Met Val Val Ala Leu Lys	
465 470 475 480	
gaa ctg tcc atc cga ggt gac ttt agg act acc gtg gaa tac ctc att	1488
Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile	
485 490 495	
aac ctc ctg gag acc gag agc ttc cag aac aac gac atc gac acc ggg	1536
Asn Leu Leu Glu Thr Glu Ser Phe Gln Asn Asn Asp Ile Asp Thr Gly	
500 505 510	



tgg ttg gac tac ctc att gct gag aaa gtg cag gag aaa ccg gat atc	1584
Trp Leu Asp Tyr Leu Ile Ala Glu Lys Val Gln Glu Lys Pro Asp Ile	
515 520 525	

atg ctt ggg gtg	1596
Met Leu Gly Val	
530	

<210> 16  
 <211> 532  
 <212> PRT  
 <213> Homo sapiens

<400> 16

Met Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe Gly Gly Asp Arg
1 5 10 15

Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys
20 25 30

Cys Met Arg Ser Ile Arg Arg Trp Ala Tyr Glu Met Phe Arg Asn Glu
35 40 45

Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu Asp Leu Lys Ala
50 55 60

Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val Pro Val Pro Gly
65 70 75 80

Gly Pro Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Val Asp Ile
85 90 95

Ala Lys Arg Ile Pro Leu Gln Ala Val Trp Ala Gly Trp Gly His Ala
100 105 110

Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Cys Lys Asn Gly Val Ala
115 120 125

Phe Leu Gly Pro Pro Ser Glu Ala Met Trp Ala Leu Gly Asp Lys Ile
130 135 140

Ala Ser Thr Val Val Ala Gln Thr Leu Gln Val Pro Thr Leu Pro Arg
145 150 155 160

Ser Gly Ser Gly Leu Thr Val Glu Trp Thr Glu Asp Asp Leu Gln Gln
165 170 175

Gly Lys Arg Ile Ser Val Pro Glu Asp Val Tyr Asp Lys Gly Cys Val
---

180	185	190
Lys Asp Val Asp Glu Gly Leu Glu Ala Ala Glu Arg Ile Gly Phe Pro		
195	200	205
Leu Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Lys		
210	215	220
Ala Glu Ser Ala Glu Asp Phe Pro Ile Leu Phe Arg Gln Val Gln Ser		
225	230	240
Glu Ile Pro Gly Ser Pro Ile Phe Leu Met Lys Leu Ala Gln His Ala		
	245	250
		255
Arg His Leu Glu Val Gln Ile Leu Ala Asp Gln Tyr Gly Asn Ala Val		
	260	265
		270
Ser Leu Phe Gly Arg Asp Cys Ser Ile Gln Arg Arg His Gln Lys Ile		
	275	280
		285
Val Glu Glu Ala Pro Ala Thr Ile Ala Pro Leu Ala Ile Phe Glu Phe		
	290	295
		300
Met Glu Gln Cys Ala Ile Arg Leu Ala Lys Thr Val Gly Tyr Val Ser		
305	310	315
		320
Ala Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp Gly Ser Phe His Phe		
	325	330
		335
Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Cys Thr Glu Met		
	340	345
		350
Ile Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala Met Gly		
	355	360
		365
Val Pro Leu His Arg Leu Lys Asp Ile Arg Leu Leu Tyr Gly Glu Ser		
	370	375
		380
Pro Trp Gly Val Thr Pro Ile Ser Phe Glu Thr Pro Ser Asn Pro Pro		
385	390	395
		400
Leu Ala Arg Gly His Val Ile Ala Ala Arg Ile Thr Ser Glu Asn Pro		
	405	410
		415
Asp Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu Leu Asn Phe		
	420	425
		430

Arg Ser Ser Lys Asn Val Trp Gly Tyr Phe Ser Val Ala Ala Thr Gly  
 435 440 445

Gly Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys Phe Ser Trp  
 450 455 460

Gly Glu Asn Arg Lys Glu Ala Ile Ser Asn Met Val Val Ala Leu Lys  
 465 470 475 480

Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile  
 485 490 495

Asn Leu Leu Glu Thr Glu Ser Phe Gln Asn Asn Asp Ile Asp Thr Gly  
 500 505 510

Trp Leu Asp Tyr Leu Ile Ala Glu Lys Val Gln Glu Lys Pro Asp Ile  
 515 520 525

Met Leu Gly Val  
 530

<210> 17  
 <211> 554  
 <212> PRT  
 <213> Ustilago maydis

<220>  
 <221> MISC\_FEATURE  
 <222> (1)..(554)  
 <223> N-terminal deleted Ustilago ACCase BC domain (AAs 7-560)

<400> 17

Lys Ala Val Ser Gln Phe Ile Gly Gly Asn Pro Leu Glu Thr Ala Pro  
 1 5 10 15

Ala Ser Pro Val Ala Asp Phe Ile Arg Lys Gln Gly Gly His Ser Val  
 20 25 30

Ile Thr Lys Val Leu Ile Cys Asn Asn Gly Ile Ala Ala Val Lys Glu  
 35 40 45

Ile Arg Ser Ile Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu Arg  
 50 55 60

Ala Ile Glu Phe Thr Val Met Ala Thr Pro Glu Asp Leu Lys Val Asn  
 65 70 75 80

Ala Asp Tyr Ile Arg Met Ala Asp Gln Tyr Val Glu Val Pro Gly Gly  
                     85                    90                    95

Ser Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile Val Asp Val Ala  
                     100                    105                    110

Glu Arg Ala Gly Val His Ala Val Trp Ala Gly Trp Gly His Ala Ser  
             115                    120                    125

Glu Asn Pro Arg Leu Pro Glu Ser Leu Ala Ala Ser Lys His Lys Ile  
             130                    135                    140

Ile Phe Ile Gly Pro Pro Gly Ser Ala Met Arg Ser Leu Gly Asp Lys  
 145                    150                    155                    160

Ile Ser Ser Thr Ile Val Ala Gln His Ala Asp Val Pro Cys Met Pro  
                     165                    170                    175

Trp Ser Gly Thr Gly Ile Lys Glu Thr Met Met Ser Asp Gln Gly Phe  
             180                    185                    190

Leu Thr Val Ser Asp Asp Val Tyr Gln Gln Ala Cys Ile His Thr Ala  
             195                    200                    205

Glu Glu Gly Leu Glu Lys Ala Glu Lys Ile Gly Tyr Pro Val Met Ile  
             210                    215                    220

Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Lys Cys Thr Asn  
 225                    230                    235                    240

Gly Glu Glu Phe Lys Gln Leu Tyr Asn Ala Val Leu Gly Glu Val Pro  
                     245                    250                    255

Gly Ser Pro Val Phe Val Met Lys Leu Ala Gly Gln Ala Arg His Leu  
             260                    265                    270

Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn Ala Ile Ser Ile Phe  
             275                    280                    285

Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile Ile Glu Glu  
             290                    295                    300

Ala Pro Val Thr Ile Ala Pro Glu Asp Ala Arg Glu Ser Met Glu Lys  
 305                    310                    315                    320

Ala Ala Val Arg Leu Ala Lys Leu Val Gly Tyr Val Ser Ala Gly Thr  
 325 330 335

Val Glu Trp Leu Tyr Ser Pro Glu Ser Gly Glu Phe Ala Phe Leu Glu  
 340 345 350

Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr Thr Glu Met Val Ser  
 355 360 365

Gly Val Asn Ile Pro Ala Ala Gln Leu Gln Val Ala Met Gly Ile Pro  
 370 375 380

Leu Tyr Ser Ile Arg Asp Ile Arg Thr Leu Tyr Gly Met Asp Pro Arg  
 385 390 395 400

Gly Asn Glu Val Ile Asp Phe Asp Phe Ser Ser Pro Glu Ser Phe Lys  
 405 410 415

Thr Gln Arg Lys Pro Gln Pro Gln Gly His Val Val Ala Cys Arg Ile  
 420 425 430

Thr Ala Glu Asn Pro Asp Thr Gly Phe Lys Pro Gly Met Gly Ala Leu  
 435 440 445

Thr Glu Leu Asn Phe Arg Ser Ser Thr Ser Thr Trp Gly Tyr Phe Ser  
 450 455 460

Val Gly Thr Ser Gly Ala Leu His Glu Tyr Ala Asp Ser Gln Phe Gly  
 465 470 475 480

His Ile Phe Ala Tyr Gly Ala Asp Arg Ser Glu Ala Arg Lys Gln Met  
 485 490 495

Val Ile Ser Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr  
 500 505 510

Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Asp Ala Phe Glu Ser Asn  
 515 520 525

Lys Ile Thr Thr Gly Trp Leu Asp Gly Leu Ile Gln Asp Arg Leu Thr  
 530 535 540

Ala Glu Arg Pro Pro Ala Asp Leu Ala Val  
 545 550

<210> 18  
 <211> 549  
 <212> PRT  
 <213> Ustilago maydis

<220>  
 <221> MISC\_FEATURE  
 <222> (1)..(549)  
 <223> N-terminal deleted Ustilago ACCase BC domain (AAs 12-560)

<400> 18

Phe Ile Gly Gly Asn Pro Leu Glu Thr Ala Pro Ala Ser Pro Val Ala  
 1 5 10 15

Asp Phe Ile Arg Lys Gln Gly Gly His Ser Val Ile Thr Lys Val Leu  
 20 25 30

Ile Cys Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Ile Arg  
 35 40 45

Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu Arg Ala Ile Glu Phe Thr  
 50 55 60

Val Met Ala Thr Pro Glu Asp Leu Lys Val Asn Ala Asp Tyr Ile Arg  
 65 70 75 80

Met Ala Asp Gln Tyr Val Glu Val Pro Gly Gly Ser Asn Asn Asn Asn  
 85 90 95

Tyr Ala Asn Val Asp Leu Ile Val Asp Val Ala Glu Arg Ala Gly Val  
 100 105 110

His Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Arg Leu  
 115 120 125

Pro Glu Ser Leu Ala Ala Ser Lys His Lys Ile Ile Phe Ile Gly Pro  
 130 135 140

Pro Gly Ser Ala Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile  
 145 150 155 160

Val Ala Gln His Ala Asp Val Pro Cys Met Pro Trp Ser Gly Thr Gly  
 165 170 175

Ile Lys Glu Thr Met Met Ser Asp Gln Gly Phe Leu Thr Val Ser Asp  
 180 185 190

Asp Val Tyr Gln Gln Ala Cys Ile His Thr Ala Glu Glu Gly Leu Glu  
 195 200 205

Lys Ala Glu Lys Ile Gly Tyr Pro Val Met Ile Lys Ala Ser Glu Gly  
 210 215 220

Gly Gly Gly Lys Gly Ile Arg Lys Cys Thr Asn Gly Glu Glu Phe Lys  
 225 230 235 240

Gln Leu Tyr Asn Ala Val Leu Gly Glu Val Pro Gly Ser Pro Val Phe  
 245 250 255

Val Met Lys Leu Ala Gly Gln Ala Arg His Leu Glu Val Gln Leu Leu  
 260 265 270

Ala Asp Gln Tyr Gly Asn Ala Ile Ser Ile Phe Gly Arg Asp Cys Ser  
 275 280 285

Val Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala Pro Val Thr Ile  
 290 295 300

Ala Pro Glu Asp Ala Arg Glu Ser Met Glu Lys Ala Ala Val Arg Leu  
 305 310 315 320

Ala Lys Leu Val Gly Tyr Val Ser Ala Gly Thr Val Glu Trp Leu Tyr  
 325 330 335

Ser Pro Glu Ser Gly Glu Phe Ala Phe Leu Glu Leu Asn Pro Arg Leu  
 340 345 350

Gln Val Glu His Pro Thr Thr Glu Met Val Ser Gly Val Asn Ile Pro  
 355 360 365

Ala Ala Gln Leu Gln Val Ala Met Gly Ile Pro Leu Tyr Ser Ile Arg  
 370 375 380

Asp Ile Arg Thr Leu Tyr Gly Met Asp Pro Arg Gly Asn Glu Val Ile  
 385 390 395 400

Asp Phe Asp Phe Ser Ser Pro Glu Ser Phe Lys Thr Gln Arg Lys Pro  
 405 410 415

Gln Pro Gln Gly His Val Val Ala Cys Arg Ile Thr Ala Glu Asn Pro  
 420 425 430

Asp Thr Gly Phe Lys Pro Gly Met Gly Ala Leu Thr Glu Leu Asn Phe

435                      440                      445  
 Arg Ser Ser Thr Ser Thr Trp Gly Tyr Phe Ser Val Gly Thr Ser Gly  
     450                      455                      460  
  
 Ala Leu His Glu Tyr Ala Asp Ser Gln Phe Gly His Ile Phe Ala Tyr  
     465                      470                      475                      480  
  
 Gly Ala Asp Arg Ser Glu Ala Arg Lys Gln Met Val Ile Ser Leu Lys  
                     485                      490                      495  
  
 Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile  
                     500                      505                      510  
  
 Lys Leu Leu Glu Thr Asp Ala Phe Glu Ser Asn Lys Ile Thr Thr Gly  
                     515                      520                      525  
  
 Trp Leu Asp Gly Leu Ile Gln Asp Arg Leu Thr Ala Glu Arg Pro Pro  
     530                      535                      540  
  
 Ala Asp Leu Ala Val  
 545  
  
 <210> 19  
 <211> 539  
 <212> PRT  
 <213> Ustilago maydis  
  
 <220>  
 <221> MISC\_FEATURE  
 <222> (1)..(539)  
 <223> N-terminal deleted Ustilago ACCse BC domain (AAs 22-560)  
  
 <400> 19  
  
 Pro Ala Ser Pro Val Ala Asp Phe Ile Arg Lys Gln Gly Gly His Ser  
 1                      5                      10                      15  
  
 Val Ile Thr Lys Val Leu Ile Cys Asn Asn Gly Ile Ala Ala Val Lys  
                     20                      25                      30  
  
 Glu Ile Arg Ser Ile Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu  
     35                      40                      45  
  
 Arg Ala Ile Glu Phe Thr Val Met Ala Thr Pro Glu Asp Leu Lys Val  
     50                      55                      60  
  
 Asn Ala Asp Tyr Ile Arg Met Ala Asp Gln Tyr Val Glu Val Pro Gly



65		70		75		80
Gly Ser Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile Val Asp Val						
		85		90		95
Ala Glu Arg Ala Gly Val His Ala Val Trp Ala Gly Trp Gly His Ala						
		100		105		110
Ser Glu Asn Pro Arg Leu Pro Glu Ser Leu Ala Ala Ser Lys His Lys						
		115		120		125
Ile Ile Phe Ile Gly Pro Pro Gly Ser Ala Met Arg Ser Leu Gly Asp						
		130		135		140
Lys Ile Ser Ser Thr Ile Val Ala Gln His Ala Asp Val Pro Cys Met						
		145		150		155
Pro Trp Ser Gly Thr Gly Ile Lys Glu Thr Met Met Ser Asp Gln Gly						
		165		170		175
Phe Leu Thr Val Ser Asp Asp Val Tyr Gln Gln Ala Cys Ile His Thr						
		180		185		190
Ala Glu Glu Gly Leu Glu Lys Ala Glu Lys Ile Gly Tyr Pro Val Met						
		195		200		205
Ile Lys Ala Ser Glu Gly Gly Gly Lys Gly Ile Arg Lys Cys Thr						
		210		215		220
Asn Gly Glu Glu Phe Lys Gln Leu Tyr Asn Ala Val Leu Gly Glu Val						
		225		230		235
Pro Gly Ser Pro Val Phe Val Met Lys Leu Ala Gly Gln Ala Arg His						
		245		250		255
Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn Ala Ile Ser Ile						
		260		265		270
Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile Ile Glu						
		275		280		285
Glu Ala Pro Val Thr Ile Ala Pro Glu Asp Ala Arg Glu Ser Met Glu						
		290		295		300
Lys Ala Ala Val Arg Leu Ala Lys Leu Val Gly Tyr Val Ser Ala Gly						
		305		310		315
						320

Thr Val Glu Trp Leu Tyr Ser Pro Glu Ser Gly Glu Phe Ala Phe Leu  
 325 330 335

Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr Thr Glu Met Val  
 340 345 350

Ser Gly Val Asn Ile Pro Ala Ala Gln Leu Gln Val Ala Met Gly Ile  
 355 360 365

Pro Leu Tyr Ser Ile Arg Asp Ile Arg Thr Leu Tyr Gly Met Asp Pro  
 370 375 380

Arg Gly Asn Glu Val Ile Asp Phe Asp Phe Ser Ser Pro Glu Ser Phe  
 385 390 395 400

Lys Thr Gln Arg Lys Pro Gln Pro Gln Gly His Val Val Ala Cys Arg  
 405 410 415

Ile Thr Ala Glu Asn Pro Asp Thr Gly Phe Lys Pro Gly Met Gly Ala  
 420 425 430

Leu Thr Glu Leu Asn Phe Arg Ser Ser Thr Ser Thr Trp Gly Tyr Phe  
 435 440 445

Ser Val Gly Thr Ser Gly Ala Leu His Glu Tyr Ala Asp Ser Gln Phe  
 450 455 460

Gly His Ile Phe Ala Tyr Gly Ala Asp Arg Ser Glu Ala Arg Lys Gln  
 465 470 475 480

Met Val Ile Ser Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr  
 485 490 495

Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Asp Ala Phe Glu Ser  
 500 505 510

Asn Lys Ile Thr Thr Gly Trp Leu Asp Gly Leu Ile Gln Asp Arg Leu  
 515 520 525

Thr Ala Glu Arg Pro Pro Ala Asp Leu Ala Val  
 530 535

<210> 20  
 <211> 529  
 <212> PRT

<213> Ustilago maydis

<220>

<221> MISC\_FEATURE

<222> (1)..(529)

<223> N-terminal deleted Ustilago ACCase BC domain (AAs 32-560)

<400> 20

Lys Gln Gly Gly His Ser Val Ile Thr Lys Val Leu Ile Cys Asn Asn  
1 5 10 15

Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Ile Arg Lys Trp Ala Tyr  
20 25 30

Glu Thr Phe Gly Asp Glu Arg Ala Ile Glu Phe Thr Val Met Ala Thr  
35 40 45

Pro Glu Asp Leu Lys Val Asn Ala Asp Tyr Ile Arg Met Ala Asp Gln  
50 55 60

Tyr Val Glu Val Pro Gly Gly Ser Asn Asn Asn Asn Tyr Ala Asn Val  
65 70 75 80

Asp Leu Ile Val Asp Val Ala Glu Arg Ala Gly Val His Ala Val Trp  
85 90 95

Ala Gly Trp Gly His Ala Ser Glu Asn Pro Arg Leu Pro Glu Ser Leu  
100 105 110

Ala Ala Ser Lys His Lys Ile Ile Phe Ile Gly Pro Pro Gly Ser Ala  
115 120 125

Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln His  
130 135 140

Ala Asp Val Pro Cys Met Pro Trp Ser Gly Thr Gly Ile Lys Glu Thr  
145 150 155 160

Met Met Ser Asp Gln Gly Phe Leu Thr Val Ser Asp Asp Val Tyr Gln  
165 170 175

Gln Ala Cys Ile His Thr Ala Glu Glu Gly Leu Glu Lys Ala Glu Lys  
180 185 190

Ile Gly Tyr Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys  
195 200 205

Gly Ile Arg Lys Cys Thr Asn Gly Glu Glu Phe Lys Gln Leu Tyr Asn  
 210 215 220

Ala Val Leu Gly Glu Val Pro Gly Ser Pro Val Phe Val Met Lys Leu  
 225 230 235 240

Ala Gly Gln Ala Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr  
 245 250 255

Gly Asn Ala Ile Ser Ile Phe Gly Arg Asp Cys Ser Val Gln Arg Arg  
 260 265 270

His Gln Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala Pro Glu Asp  
 275 280 285

Ala Arg Glu Ser Met Glu Lys Ala Ala Val Arg Leu Ala Lys Leu Val  
 290 295 300

Gly Tyr Val Ser Ala Gly Thr Val Glu Trp Leu Tyr Ser Pro Glu Ser  
 305 310 315 320

Gly Glu Phe Ala Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His  
 325 330 335

Pro Thr Thr Glu Met Val Ser Gly Val Asn Ile Pro Ala Ala Gln Leu  
 340 345 350

Gln Val Ala Met Gly Ile Pro Leu Tyr Ser Ile Arg Asp Ile Arg Thr  
 355 360 365

Leu Tyr Gly Met Asp Pro Arg Gly Asn Glu Val Ile Asp Phe Asp Phe  
 370 375 380

Ser Ser Pro Glu Ser Phe Lys Thr Gln Arg Lys Pro Gln Pro Gln Gly  
 385 390 395 400

His Val Val Ala Cys Arg Ile Thr Ala Glu Asn Pro Asp Thr Gly Phe  
 405 410 415

Lys Pro Gly Met Gly Ala Leu Thr Glu Leu Asn Phe Arg Ser Ser Thr  
 420 425 430

Ser Thr Trp Gly Tyr Phe Ser Val Gly Thr Ser Gly Ala Leu His Glu  
 435 440 445

Tyr Ala Asp Ser Gln Phe Gly His Ile Phe Ala Tyr Gly Ala Asp Arg  
 450 455 460

Ser Glu Ala Arg Lys Gln Met Val Ile Ser Leu Lys Glu Leu Ser Ile  
 465 470 475 480

Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu  
 485 490 495

Thr Asp Ala Phe Glu Ser Asn Lys Ile Thr Thr Gly Trp Leu Asp Gly  
 500 505 510

Leu Ile Gln Asp Arg Leu Thr Ala Glu Arg Pro Pro Ala Asp Leu Ala  
 515 520 525

Val

<210> 21  
 <211> 519  
 <212> PRT  
 <213> Ustilago maydis

<220>  
 <221> MISC\_FEATURE  
 <222> (1)..(519)  
 <223> N-terminal deleted Ustilago ACCase BC domain (AAs 42-560)

<400> 21

Val Leu Ile Cys Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Ser  
 1 5 10 15

Ile Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu Arg Ala Ile Glu  
 20 25 30

Phe Thr Val Met Ala Thr Pro Glu Asp Leu Lys Val Asn Ala Asp Tyr  
 35 40 45

Ile Arg Met Ala Asp Gln Tyr Val Glu Val Pro Gly Gly Ser Asn Asn  
 50 55 60

Asn Asn Tyr Ala Asn Val Asp Leu Ile Val Asp Val Ala Glu Arg Ala  
 65 70 75 80

Gly Val His Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro  
 85 90 95

Arg Leu Pro Glu Ser Leu Ala Ala Ser Lys His Lys Ile Ile Phe Ile  
 100 105 110

Gly Pro Pro Gly Ser Ala Met Arg Ser Leu Gly Asp Lys Ile Ser Ser  
 115 120 125

Thr Ile Val Ala Gln His Ala Asp Val Pro Cys Met Pro Trp Ser Gly  
 130 135 140

Thr Gly Ile Lys Glu Thr Met Met Ser Asp Gln Gly Phe Leu Thr Val  
 145 150 155 160

Ser Asp Asp Val Tyr Gln Gln Ala Cys Ile His Thr Ala Glu Glu Gly  
 165 170 175

Leu Glu Lys Ala Glu Lys Ile Gly Tyr Pro Val Met Ile Lys Ala Ser  
 180 185 190

Glu Gly Gly Gly Gly Lys Gly Ile Arg Lys Cys Thr Asn Gly Glu Glu  
 195 200 205

Phe Lys Gln Leu Tyr Asn Ala Val Leu Gly Glu Val Pro Gly Ser Pro  
 210 215 220

Val Phe Val Met Lys Leu Ala Gly Gln Ala Arg His Leu Glu Val Gln  
 225 230 235 240

Leu Leu Ala Asp Gln Tyr Gly Asn Ala Ile Ser Ile Phe Gly Arg Asp  
 245 250 255

Cys Ser Val Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala Pro Val  
 260 265 270

Thr Ile Ala Pro Glu Asp Ala Arg Glu Ser Met Glu Lys Ala Ala Val  
 275 280 285

Arg Leu Ala Lys Leu Val Gly Tyr Val Ser Ala Gly Thr Val Glu Trp  
 290 295 300

Leu Tyr Ser Pro Glu Ser Gly Glu Phe Ala Phe Leu Glu Leu Asn Pro  
 305 310 315 320

Arg Leu Gln Val Glu His Pro Thr Thr Glu Met Val Ser Gly Val Asn  
 325 330 335

Ile Pro Ala Ala Gln Leu Gln Val Ala Met Gly Ile Pro Leu Tyr Ser

[illegible]

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<210> 22
<211> 554
<212> PRT
<213> Ustilago maydis
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<220>
<221> MISC_FEATURE
<222> (1)..(554)
<223> C-terminal deleted Ustilago ACCase BC domain (AAs 2-555)

<400> 22

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Pro Pro Pro Asp His Lys Ala Val Ser Gln Phe Ile Gly Gly Asn Pro

1	5	10	15												
Leu	Glu	Thr	Ala	Pro	Ala	Ser	Pro	Val	Ala	Asp	Phe	Ile	Arg	Lys	Gln
			20					25					30		
Gly	Gly	His	Ser	Val	Ile	Thr	Lys	Val	Leu	Ile	Cys	Asn	Asn	Gly	Ile
		35					40					45			
Ala	Ala	Val	Lys	Glu	Ile	Arg	Ser	Ile	Arg	Lys	Trp	Ala	Tyr	Glu	Thr
		50				55					60				
Phe	Gly	Asp	Glu	Arg	Ala	Ile	Glu	Phe	Thr	Val	Met	Ala	Thr	Pro	Glu
65					70					75				80	
Asp	Leu	Lys	Val	Asn	Ala	Asp	Tyr	Ile	Arg	Met	Ala	Asp	Gln	Tyr	Val
			85						90					95	
Glu	Val	Pro	Gly	Gly	Ser	Asn	Asn	Asn	Asn	Tyr	Ala	Asn	Val	Asp	Leu
			100					105					110		
Ile	Val	Asp	Val	Ala	Glu	Arg	Ala	Gly	Val	His	Ala	Val	Trp	Ala	Gly
		115					120					125			
Trp	Gly	His	Ala	Ser	Glu	Asn	Pro	Arg	Leu	Pro	Glu	Ser	Leu	Ala	Ala
	130					135					140				
Ser	Lys	His	Lys	Ile	Ile	Phe	Ile	Gly	Pro	Pro	Gly	Ser	Ala	Met	Arg
145				150						155				160	
Ser	Leu	Gly	Asp	Lys	Ile	Ser	Ser	Thr	Ile	Val	Ala	Gln	His	Ala	Asp
			165						170				175		
Val	Pro	Cys	Met	Pro	Trp	Ser	Gly	Thr	Gly	Ile	Lys	Glu	Thr	Met	Met
			180					185					190		
Ser	Asp	Gln	Gly	Phe	Leu	Thr	Val	Ser	Asp	Asp	Val	Tyr	Gln	Gln	Ala
		195					200					205			
Cys	Ile	His	Thr	Ala	Glu	Glu	Gly	Leu	Glu	Lys	Ala	Glu	Lys	Ile	Gly
	210					215					220				
Tyr	Pro	Val	Met	Ile	Lys	Ala	Ser	Glu	Gly	Gly	Gly	Gly	Lys	Gly	Ile
225					230					235				240	
Arg	Lys	Cys	Thr	Asn	Gly	Glu	Glu	Phe	Lys	Gln	Leu	Tyr	Asn	Ala	Val
				245					250					255	



Leu Gly Glu Val Pro Gly Ser Pro Val Phe Val Met Lys Leu Ala Gly  
260 265 270

Gln Ala Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn  
275 280 285

Ala Ile Ser Ile Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln  
290 295 300

Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala Pro Glu Asp Ala Arg  
305 310 315 320

Glu Ser Met Glu Lys Ala Ala Val Arg Leu Ala Lys Leu Val Gly Tyr  
325 330 335

Val Ser Ala Gly Thr Val Glu Trp Leu Tyr Ser Pro Glu Ser Gly Glu  
340 345 350

Phe Ala Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr  
355 360 365

Thr Glu Met Val Ser Gly Val Asn Ile Pro Ala Ala Gln Leu Gln Val  
370 375 380

Ala Met Gly Ile Pro Leu Tyr Ser Ile Arg Asp Ile Arg Thr Leu Tyr  
385 390 395 400

Gly Met Asp Pro Arg Gly Asn Glu Val Ile Asp Phe Asp Phe Ser Ser  
405 410 415

Pro Glu Ser Phe Lys Thr Gln Arg Lys Pro Gln Pro Gln Gly His Val  
420 425 430

Val Ala Cys Arg Ile Thr Ala Glu Asn Pro Asp Thr Gly Phe Lys Pro  
435 440 445

Gly Met Gly Ala Leu Thr Glu Leu Asn Phe Arg Ser Ser Thr Ser Thr  
450 455 460

Trp Gly Tyr Phe Ser Val Gly Thr Ser Gly Ala Leu His Glu Tyr Ala  
465 470 475 480

Asp Ser Gln Phe Gly His Ile Phe Ala Tyr Gly Ala Asp Arg Ser Glu  
485 490 495

Ala Arg Lys Gln Met Val Ile Ser Leu Lys Glu Leu Ser Ile Arg Gly  
500 505 510

Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Asp  
515 520 525

Ala Phe Glu Ser Asn Lys Ile Thr Thr Gly Trp Leu Asp Gly Leu Ile  
530 535 540

Gln Asp Arg Leu Thr Ala Glu Arg Pro Pro  
545 550

<210> 23  
<211> 549  
<212> PRT  
<213> Ustilago maydis

<220>  
<221> MISC\_FEATURE  
<222> (1)..(549)  
<223> C-terminal deleted Ustilago ACCase BC domain (AAs 2-550)

<400> 23

Pro Pro Pro Asp His Lys Ala Val Ser Gln Phe Ile Gly Gly Asn Pro  
1 5 10 15

Leu Glu Thr Ala Pro Ala Ser Pro Val Ala Asp Phe Ile Arg Lys Gln  
20 25 30

Gly Gly His Ser Val Ile Thr Lys Val Leu Ile Cys Asn Asn Gly Ile  
35 40 45

Ala Ala Val Lys Glu Ile Arg Ser Ile Arg Lys Trp Ala Tyr Glu Thr  
50 55 60

Phe Gly Asp Glu Arg Ala Ile Glu Phe Thr Val Met Ala Thr Pro Glu  
65 70 75 80

Asp Leu Lys Val Asn Ala Asp Tyr Ile Arg Met Ala Asp Gln Tyr Val  
85 90 95

Glu Val Pro Gly Gly Ser Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu  
100 105 110

Ile Val Asp Val Ala Glu Arg Ala Gly Val His Ala Val Trp Ala Gly  
115 120 125

Trp Gly His Ala Ser Glu Asn Pro Arg Leu Pro Glu Ser Leu Ala Ala  
 130 135 140

Ser Lys His Lys Ile Ile Phe Ile Gly Pro Pro Gly Ser Ala Met Arg  
 145 150 155 160

Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln His Ala Asp  
 165 170 175

Val Pro Cys Met Pro Trp Ser Gly Thr Gly Ile Lys Glu Thr Met Met  
 180 185 190

Ser Asp Gln Gly Phe Leu Thr Val Ser Asp Asp Val Tyr Gln Gln Ala  
 195 200 205

Cys Ile His Thr Ala Glu Glu Gly Leu Glu Lys Ala Glu Lys Ile Gly  
 210 215 220

Tyr Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile  
 225 230 235 240

Arg Lys Cys Thr Asn Gly Glu Glu Phe Lys Gln Leu Tyr Asn Ala Val  
 245 250 255

Leu Gly Glu Val Pro Gly Ser Pro Val Phe Val Met Lys Leu Ala Gly  
 260 265 270

Gln Ala Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn  
 275 280 285

Ala Ile Ser Ile Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln  
 290 295 300

Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala Pro Glu Asp Ala Arg  
 305 310 315 320

Glu Ser Met Glu Lys Ala Ala Val Arg Leu Ala Lys Leu Val Gly Tyr  
 325 330 335

Val Ser Ala Gly Thr Val Glu Trp Leu Tyr Ser Pro Glu Ser Gly Glu  
 340 345 350

Phe Ala Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr  
 355 360 365

Thr Glu Met Val Ser Gly Val Asn Ile Pro Ala Ala Gln Leu Gln Val  
 370 375 380

Ala Met Gly Ile Pro Leu Tyr Ser Ile Arg Asp Ile Arg Thr Leu Tyr  
 385 390 395 400

Gly Met Asp Pro Arg Gly Asn Glu Val Ile Asp Phe Asp Phe Ser Ser  
 405 410 415

Pro Glu Ser Phe Lys Thr Gln Arg Lys Pro Gln Pro Gln Gly His Val  
 420 425 430

Val Ala Cys Arg Ile Thr Ala Glu Asn Pro Asp Thr Gly Phe Lys Pro  
 435 440 445

Gly Met Gly Ala Leu Thr Glu Leu Asn Phe Arg Ser Ser Thr Ser Thr  
 450 455 460

Trp Gly Tyr Phe Ser Val Gly Thr Ser Gly Ala Leu His Glu Tyr Ala  
 465 470 475 480

Asp Ser Gln Phe Gly His Ile Phe Ala Tyr Gly Ala Asp Arg Ser Glu  
 485 490 495

Ala Arg Lys Gln Met Val Ile Ser Leu Lys Glu Leu Ser Ile Arg Gly  
 500 505 510

Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Asp  
 515 520 525

Ala Phe Glu Ser Asn Lys Ile Thr Thr Gly Trp Leu Asp Gly Leu Ile  
 530 535 540

Gln Asp Arg Leu Thr  
 545

<210> 24  
 <211> 539  
 <212> PRT  
 <213> Ustilago maydis

<220>  
 <221> MISC\_FEATURE  
 <222> (1)..(539)  
 <223> C-terminal deleted Ustilago ACCase BC domain (AAs 2-540)  
 <400> 24

Pro Pro Pro Asp His Lys Ala Val Ser Gln Phe Ile Gly Gly Asn Pro  
 1 5 10 15  
 Leu Glu Thr Ala Pro Ala Ser Pro Val Ala Asp Phe Ile Arg Lys Gln  
 20 25 30  
 Gly Gly His Ser Val Ile Thr Lys Val Leu Ile Cys Asn Asn Gly Ile  
 35 40 45  
 Ala Ala Val Lys Glu Ile Arg Ser Ile Arg Lys Trp Ala Tyr Glu Thr  
 50 55 60  
 Phe Gly Asp Glu Arg Ala Ile Glu Phe Thr Val Met Ala Thr Pro Glu  
 65 70 75 80  
 Asp Leu Lys Val Asn Ala Asp Tyr Ile Arg Met Ala Asp Gln Tyr Val  
 85 90 95  
 Glu Val Pro Gly Gly Ser Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu  
 100 105 110  
 Ile Val Asp Val Ala Glu Arg Ala Gly Val His Ala Val Trp Ala Gly  
 115 120 125  
 Trp Gly His Ala Ser Glu Asn Pro Arg Leu Pro Glu Ser Leu Ala Ala  
 130 135 140  
 Ser Lys His Lys Ile Ile Phe Ile Gly Pro Pro Gly Ser Ala Met Arg  
 145 150 155 160  
 Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln His Ala Asp  
 165 170 175  
 Val Pro Cys Met Pro Trp Ser Gly Thr Gly Ile Lys Glu Thr Met Met  
 180 185 190  
 Ser Asp Gln Gly Phe Leu Thr Val Ser Asp Asp Val Tyr Gln Gln Ala  
 195 200 205  
 Cys Ile His Thr Ala Glu Glu Gly Leu Glu Lys Ala Glu Lys Ile Gly  
 210 215 220  
 Tyr Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile  
 225 230 235 240  
 Arg Lys Cys Thr Asn Gly Glu Glu Phe Lys Gln Leu Tyr Asn Ala Val

	245		250		255
Leu Gly Glu Val Pro Gly Ser Pro Val Phe Val Met Lys Leu Ala Gly	260	265	270		
Gln Ala Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn	275	280	285		
Ala Ile Ser Ile Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln	290	295	300		
Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala Pro Glu Asp Ala Arg	305	310	315	320	
Glu Ser Met Glu Lys Ala Ala Val Arg Leu Ala Lys Leu Val Gly Tyr	325	330	335		
Val Ser Ala Gly Thr Val Glu Trp Leu Tyr Ser Pro Glu Ser Gly Glu	340	345	350		
Phe Ala Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr	355	360	365		
Thr Glu Met Val Ser Gly Val Asn Ile Pro Ala Ala Gln Leu Gln Val	370	375	380		
Ala Met Gly Ile Pro Leu Tyr Ser Ile Arg Asp Ile Arg Thr Leu Tyr	385	390	395	400	
Gly Met Asp Pro Arg Gly Asn Glu Val Ile Asp Phe Asp Phe Ser Ser	405	410	415		
Pro Glu Ser Phe Lys Thr Gln Arg Lys Pro Gln Pro Gln Gly His Val	420	425	430		
Val Ala Cys Arg Ile Thr Ala Glu Asn Pro Asp Thr Gly Phe Lys Pro	435	440	445		
Gly Met Gly Ala Leu Thr Glu Leu Asn Phe Arg Ser Ser Thr Ser Thr	450	455	460		
Trp Gly Tyr Phe Ser Val Gly Thr Ser Gly Ala Leu His Glu Tyr Ala	465	470	475	480	
Asp Ser Gln Phe Gly His Ile Phe Ala Tyr Gly Ala Asp Arg Ser Glu	485	490	495		

Ala Arg Lys Gln Met Val Ile Ser Leu Lys Glu Leu Ser Ile Arg Gly  
500 505 510

Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Asp  
515 520 525

Ala Phe Glu Ser Asn Lys Ile Thr Thr Gly Trp  
530 535

<210> 25  
<211> 529  
<212> PRT  
<213> Ustilago maydis

<220>  
<221> MISC\_FEATURE  
<222> (1)..(529)  
<223> C-terminal deleted Ustilago ACCase BC domain (AAs 2-530)

<400> 25

Pro Pro Pro Asp His Lys Ala Val Ser Gln Phe Ile Gly Gly Asn Pro  
1 5 10 15

Leu Glu Thr Ala Pro Ala Ser Pro Val Ala Asp Phe Ile Arg Lys Gln  
20 25 30

Gly Gly His Ser Val Ile Thr Lys Val Leu Ile Cys Asn Asn Gly Ile  
35 40 45

Ala Ala Val Lys Glu Ile Arg Ser Ile Arg Lys Trp Ala Tyr Glu Thr  
50 55 60

Phe Gly Asp Glu Arg Ala Ile Glu Phe Thr Val Met Ala Thr Pro Glu  
65 70 75 80

Asp Leu Lys Val Asn Ala Asp Tyr Ile Arg Met Ala Asp Gln Tyr Val  
85 90 95

Glu Val Pro Gly Gly Ser Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu  
100 105 110

Ile Val Asp Val Ala Glu Arg Ala Gly Val His Ala Val Trp Ala Gly  
115 120 125

Trp Gly His Ala Ser Glu Asn Pro Arg Leu Pro Glu Ser Leu Ala Ala  
130 135 140

Ser Lys His Lys Ile Ile Phe Ile Gly Pro Pro Gly Ser Ala Met Arg  
 145 150 155 160

Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln His Ala Asp  
 165 170 175

Val Pro Cys Met Pro Trp Ser Gly Thr Gly Ile Lys Glu Thr Met Met  
 180 185 190

Ser Asp Gln Gly Phe Leu Thr Val Ser Asp Asp Val Tyr Gln Gln Ala  
 195 200 205

Cys Ile His Thr Ala Glu Glu Gly Leu Glu Lys Ala Glu Lys Ile Gly  
 210 215 220

Tyr Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile  
 225 230 235 240

Arg Lys Cys Thr Asn Gly Glu Glu Phe Lys Gln Leu Tyr Asn Ala Val  
 245 250 255

Leu Gly Glu Val Pro Gly Ser Pro Val Phe Val Met Lys Leu Ala Gly  
 260 265 270

Gln Ala Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn  
 275 280 285

Ala Ile Ser Ile Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln  
 290 295 300

Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala Pro Glu Asp Ala Arg  
 305 310 315 320

Glu Ser Met Glu Lys Ala Ala Val Arg Leu Ala Lys Leu Val Gly Tyr  
 325 330 335

Val Ser Ala Gly Thr Val Glu Trp Leu Tyr Ser Pro Glu Ser Gly Glu  
 340 345 350

Phe Ala Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr  
 355 360 365

Thr Glu Met Val Ser Gly Val Asn Ile Pro Ala Ala Gln Leu Gln Val  
 370 375 380



Ala Met Gly Ile Pro Leu Tyr Ser Ile Arg Asp Ile Arg Thr Leu Tyr  
 385 390 395 400

Gly Met Asp Pro Arg Gly Asn Glu Val Ile Asp Phe Asp Phe Ser Ser  
 405 410 415

Pro Glu Ser Phe Lys Thr Gln Arg Lys Pro Gln Pro Gln Gly His Val  
 420 425 430

Val Ala Cys Arg Ile Thr Ala Glu Asn Pro Asp Thr Gly Phe Lys Pro  
 435 440 445

Gly Met Gly Ala Leu Thr Glu Leu Asn Phe Arg Ser Ser Thr Ser Thr  
 450 455 460

Trp Gly Tyr Phe Ser Val Gly Thr Ser Gly Ala Leu His Glu Tyr Ala  
 465 470 475 480

Asp Ser Gln Phe Gly His Ile Phe Ala Tyr Gly Ala Asp Arg Ser Glu  
 485 490 495

Ala Arg Lys Gln Met Val Ile Ser Leu Lys Glu Leu Ser Ile Arg Gly  
 500 505 510

Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Asp  
 515 520 525

Ala

<210> 26  
 <211> 519  
 <212> PRT  
 <213> Ustilago maydis

<220>  
 <221> MISC\_FEATURE  
 <222> (1)..(519)  
 <223> C-terminal deleted Ustilago ACCase BC domain (AAs2-520)

<400> 26

Pro Pro Pro Asp His Lys Ala Val Ser Gln Phe Ile Gly Gly Asn Pro  
 1 5 10 15

Leu Glu Thr Ala Pro Ala Ser Pro Val Ala Asp Phe Ile Arg Lys Gln  
 20 25 30

Gly Gly His Ser Val Ile Thr Lys Val Leu Ile Cys Asn Asn Gly Ile  
 35 40 45

Ala Ala Val Lys Glu Ile Arg Ser Ile Arg Lys Trp Ala Tyr Glu Thr  
 50 55 60

Phe Gly Asp Glu Arg Ala Ile Glu Phe Thr Val Met Ala Thr Pro Glu  
 65 70 75 80

Asp Leu Lys Val Asn Ala Asp Tyr Ile Arg Met Ala Asp Gln Tyr Val  
 85 90 95

Glu Val Pro Gly Gly Ser Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu  
 100 105 110

Ile Val Asp Val Ala Glu Arg Ala Gly Val His Ala Val Trp Ala Gly  
 115 120 125

Trp Gly His Ala Ser Glu Asn Pro Arg Leu Pro Glu Ser Leu Ala Ala  
 130 135 140

Ser Lys His Lys Ile Ile Phe Ile Gly Pro Pro Gly Ser Ala Met Arg  
 145 150 155 160

Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln His Ala Asp  
 165 170 175

Val Pro Cys Met Pro Trp Ser Gly Thr Gly Ile Lys Glu Thr Met Met  
 180 185 190

Ser Asp Gln Gly Phe Leu Thr Val Ser Asp Asp Val Tyr Gln Gln Ala  
 195 200 205

Cys Ile His Thr Ala Glu Glu Gly Leu Glu Lys Ala Glu Lys Ile Gly  
 210 215 220

Tyr Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile  
 225 230 235 240

Arg Lys Cys Thr Asn Gly Glu Glu Phe Lys Gln Leu Tyr Asn Ala Val  
 245 250 255

Leu Gly Glu Val Pro Gly Ser Pro Val Phe Val Met Lys Leu Ala Gly  
 260 265 270

Gln Ala Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn  
 275 280 285

Ala Ile Ser Ile Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln  
 290 295 300

Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala Pro Glu Asp Ala Arg  
 305 310 315 320

Glu Ser Met Glu Lys Ala Ala Val Arg Leu Ala Lys Leu Val Gly Tyr  
 325 330 335

Val Ser Ala Gly Thr Val Glu Trp Leu Tyr Ser Pro Glu Ser Gly Glu  
 340 345 350

Phe Ala Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr  
 355 360 365

Thr Glu Met Val Ser Gly Val Asn Ile Pro Ala Ala Gln Leu Gln Val  
 370 375 380

Ala Met Gly Ile Pro Leu Tyr Ser Ile Arg Asp Ile Arg Thr Leu Tyr  
 385 390 395 400

Gly Met Asp Pro Arg Gly Asn Glu Val Ile Asp Phe Asp Phe Ser Ser  
 405 410 415

Pro Glu Ser Phe Lys Thr Gln Arg Lys Pro Gln Pro Gln Gly His Val  
 420 425 430

Val Ala Cys Arg Ile Thr Ala Glu Asn Pro Asp Thr Gly Phe Lys Pro  
 435 440 445

Gly Met Gly Ala Leu Thr Glu Leu Asn Phe Arg Ser Ser Thr Ser Thr  
 450 455 460

Trp Gly Tyr Phe Ser Val Gly Thr Ser Gly Ala Leu His Glu Tyr Ala  
 465 470 475 480

Asp Ser Gln Phe Gly His Ile Phe Ala Tyr Gly Ala Asp Arg Ser Glu  
 485 490 495

Ala Arg Lys Gln Met Val Ile Ser Leu Lys Glu Leu Ser Ile Arg Gly  
 500 505 510

Asp Phe Arg Thr Thr Val Glu

515

<210> 27  
<211> 554  
<212> PRT  
<213> Ustilago maydis

<220>  
<221> MISC\_FEATURE  
<222> (1)..(554)  
<223> N- and C-terminal deleted Ustilago ACCase BC domain (AAs 4-547)

<400> 27

Pro Asp His Lys Ala Val Ser Gln Phe Ile Gly Gly Asn Pro Leu Glu  
1 5 10 15

Thr Ala Pro Ala Ser Pro Val Ala Asp Phe Ile Arg Lys Gln Gly Gly  
20 25 30

His Ser Val Ile Thr Lys Val Leu Ile Cys Asn Asn Gly Ile Ala Ala  
35 40 45

Val Lys Glu Ile Arg Ser Ile Arg Lys Trp Ala Tyr Glu Thr Phe Gly  
50 55 60

Asp Glu Arg Ala Ile Glu Phe Thr Val Met Ala Thr Pro Glu Asp Leu  
65 70 75 80

Lys Val Asn Ala Asp Tyr Ile Arg Met Ala Asp Gln Tyr Val Glu Val  
85 90 95

Pro Gly Gly Ser Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile Val  
100 105 110

Asp Val Ala Glu Arg Ala Gly Val His Ala Val Trp Ala Gly Trp Gly  
115 120 125

His Ala Ser Glu Asn Pro Arg Leu Pro Glu Ser Leu Ala Ala Ser Lys  
130 135 140

His Lys Ile Ile Phe Ile Gly Pro Pro Gly Ser Ala Met Arg Ser Leu  
145 150 155 160

Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln His Ala Asp Val Pro  
165 170 175

Cys Met Pro Trp Ser Gly Thr Gly Ile Lys Glu Thr Met Met Ser Asp

180	185	190
Gln Gly Phe Leu Thr Val Ser Asp Asp Val Tyr Gln Gln Ala Cys Ile		
195	200	205
His Thr Ala Glu Glu Gly Leu Glu Lys Ala Glu Lys Ile Gly Tyr Pro		
210	215	220
Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Lys		
225	230	235
Cys Thr Asn Gly Glu Glu Phe Lys Gln Leu Tyr Asn Ala Val Leu Gly		
245	250	255
Glu Val Pro Gly Ser Pro Val Phe Val Met Lys Leu Ala Gly Gln Ala		
260	265	270
Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn Ala Ile		
275	280	285
Ser Ile Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile		
290	295	300
Ile Glu Glu Ala Pro Val Thr Ile Ala Pro Glu Asp Ala Arg Glu Ser		
305	310	315
Met Glu Lys Ala Ala Val Arg Leu Ala Lys Leu Val Gly Tyr Val Ser		
325	330	335
Ala Gly Thr Val Glu Trp Leu Tyr Ser Pro Glu Ser Gly Glu Phe Ala		
340	345	350
Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr Thr Glu		
355	360	365
Met Val Ser Gly Val Asn Ile Pro Ala Ala Gln Leu Gln Val Ala Met		
370	375	380
Gly Ile Pro Leu Tyr Ser Ile Arg Asp Ile Arg Thr Leu Tyr Gly Met		
385	390	395
Asp Pro Arg Gly Asn Glu Val Ile Asp Phe Asp Phe Ser Ser Pro Glu		
405	410	415
Ser Phe Lys Thr Gln Arg Lys Pro Gln Pro Gln Gly His Val Val Ala		
420	425	430

Cys Arg Ile Thr Ala Glu Asn Pro Asp Thr Gly Phe Lys Pro Gly Met  
 435 440 445

Gly Ala Leu Thr Glu Leu Asn Phe Arg Ser Ser Thr Ser Thr Trp Gly  
 450 455 460

Tyr Phe Ser Val Gly Thr Ser Gly Ala Leu His Glu Tyr Ala Asp Ser  
 465 470 475 480

Gln Phe Gly His Ile Phe Ala Tyr Gly Ala Asp Arg Ser Glu Ala Arg  
 485 490 495

Lys Gln Met Val Ile Ser Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe  
 500 505 510

Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Asp Ala Phe  
 515 520 525

Glu Ser Asn Lys Ile Thr Thr Gly Trp Leu Asp Gly Leu Ile Gln Asp  
 530 535 540

Arg Leu Thr Ala Glu Arg Pro Pro Ala Asp  
 545 550

<210> 28  
 <211> 549  
 <212> PRT  
 <213> Ustilago maydis

<220>  
 <221> MISC\_FEATURE  
 <222> (1)..(549)  
 <223> N- and C-terminal deleted Ustilago ACCase BC domain (AAs 7-555)

<400> 28

Lys Ala Val Ser Gln Phe Ile Gly Gly Asn Pro Leu Glu Thr Ala Pro  
 1 5 10 15

Ala Ser Pro Val Ala Asp Phe Ile Arg Lys Gln Gly Gly His Ser Val  
 20 25 30

Ile Thr Lys Val Leu Ile Cys Asn Asn Gly Ile Ala Ala Val Lys Glu  
 35 40 45

Ile Arg Ser Ile Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu Arg  
 50 55 60

Ala Ile Glu Phe Thr Val Met Ala Thr Pro Glu Asp Leu Lys Val Asn  
 65 70 75 80

Ala Asp Tyr Ile Arg Met Ala Asp Gln Tyr Val Glu Val Pro Gly Gly  
 85 90 95

Ser Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile Val Asp Val Ala  
 100 105 110

Glu Arg Ala Gly Val His Ala Val Trp Ala Gly Trp Gly His Ala Ser  
 115 120 125

Glu Asn Pro Arg Leu Pro Glu Ser Leu Ala Ala Ser Lys His Lys Ile  
 130 135 140

Ile Phe Ile Gly Pro Pro Gly Ser Ala Met Arg Ser Leu Gly Asp Lys  
 145 150 155 160

Ile Ser Ser Thr Ile Val Ala Gln His Ala Asp Val Pro Cys Met Pro  
 165 170 175

Trp Ser Gly Thr Gly Ile Lys Glu Thr Met Met Ser Asp Gln Gly Phe  
 180 185 190

Leu Thr Val Ser Asp Asp Val Tyr Gln Gln Ala Cys Ile His Thr Ala  
 195 200 205

Glu Glu Gly Leu Glu Lys Ala Glu Lys Ile Gly Tyr Pro Val Met Ile  
 210 215 220

Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Lys Cys Thr Asn  
 225 230 235 240

Gly Glu Glu Phe Lys Gln Leu Tyr Asn Ala Val Leu Gly Glu Val Pro  
 245 250 255

Gly Ser Pro Val Phe Val Met Lys Leu Ala Gly Gln Ala Arg His Leu  
 260 265 270

Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn Ala Ile Ser Ile Phe  
 275 280 285

Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile Ile Glu Glu  
 290 295 300

Ala Pro Val Thr Ile Ala Pro Glu Asp Ala Arg Glu Ser Met Glu Lys  
 305 310 315 320

Ala Ala Val Arg Leu Ala Lys Leu Val Gly Tyr Val Ser Ala Gly Thr  
 325 330 335

Val Glu Trp Leu Tyr Ser Pro Glu Ser Gly Glu Phe Ala Phe Leu Glu  
 340 345 350

Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr Thr Glu Met Val Ser  
 355 360 365

Gly Val Asn Ile Pro Ala Ala Gln Leu Gln Val Ala Met Gly Ile Pro  
 370 375 380

Leu Tyr Ser Ile Arg Asp Ile Arg Thr Leu Tyr Gly Met Asp Pro Arg  
 385 390 395 400

Gly Asn Glu Val Ile Asp Phe Asp Phe Ser Ser Pro Glu Ser Phe Lys  
 405 410 415

Thr Gln Arg Lys Pro Gln Pro Gln Gly His Val Val Ala Cys Arg Ile  
 420 425 430

Thr Ala Glu Asn Pro Asp Thr Gly Phe Lys Pro Gly Met Gly Ala Leu  
 435 440 445

Thr Glu Leu Asn Phe Arg Ser Ser Thr Ser Thr Trp Gly Tyr Phe Ser  
 450 455 460

Val Gly Thr Ser Gly Ala Leu His Glu Tyr Ala Asp Ser Gln Phe Gly  
 465 470 475 480

His Ile Phe Ala Tyr Gly Ala Asp Arg Ser Glu Ala Arg Lys Gln Met  
 485 490 495

Val Ile Ser Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr  
 500 505 510

Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Asp Ala Phe Glu Ser Asn  
 515 520 525

Lys Ile Thr Thr Gly Trp Leu Asp Gly Leu Ile Gln Asp Arg Leu Thr  
 530 535 540



Ala Glu Arg Pro Pro  
545

<210> 29  
<211> 539  
<212> PRT  
<213> Ustilago maydis

<220>  
<221> MISC\_FEATURE  
<222> (1)..(539)  
<223> N- and C-terminal deleted Ustilago ACCase BC domain (AAs 12-550)  
  
<400> 29

Phe Ile Gly Gly Asn Pro Leu Glu Thr Ala Pro Ala Ser Pro Val Ala  
1 5 10 15

Asp Phe Ile Arg Lys Gln Gly Gly His Ser Val Ile Thr Lys Val Leu  
20 25 30

Ile Cys Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Ile Arg  
35 40 45

Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu Arg Ala Ile Glu Phe Thr  
50 55 60

Val Met Ala Thr Pro Glu Asp Leu Lys Val Asn Ala Asp Tyr Ile Arg  
65 70 75 80

Met Ala Asp Gln Tyr Val Glu Val Pro Gly Gly Ser Asn Asn Asn Asn  
85 90 95

Tyr Ala Asn Val Asp Leu Ile Val Asp Val Ala Glu Arg Ala Gly Val  
100 105 110

His Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Arg Leu  
115 120 125

Pro Glu Ser Leu Ala Ala Ser Lys His Lys Ile Ile Phe Ile Gly Pro  
130 135 140

Pro Gly Ser Ala Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile  
145 150 155 160

Val Ala Gln His Ala Asp Val Pro Cys Met Pro Trp Ser Gly Thr Gly  
165 170 175

Ile Lys Glu Thr Met Met Ser Asp Gln Gly Phe Leu Thr Val Ser Asp  
 180 185 190

Asp Val Tyr Gln Gln Ala Cys Ile His Thr Ala Glu Glu Gly Leu Glu  
 195 200 205

Lys Ala Glu Lys Ile Gly Tyr Pro Val Met Ile Lys Ala Ser Glu Gly  
 210 215 220

Gly Gly Gly Lys Gly Ile Arg Lys Cys Thr Asn Gly Glu Glu Phe Lys  
 225 230 235 240

Gln Leu Tyr Asn Ala Val Leu Gly Glu Val Pro Gly Ser Pro Val Phe  
 245 250 255

Val Met Lys Leu Ala Gly Gln Ala Arg His Leu Glu Val Gln Leu Leu  
 260 265 270

Ala Asp Gln Tyr Gly Asn Ala Ile Ser Ile Phe Gly Arg Asp Cys Ser  
 275 280 285

Val Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala Pro Val Thr Ile  
 290 295 300

Ala Pro Glu Asp Ala Arg Glu Ser Met Glu Lys Ala Ala Val Arg Leu  
 305 310 315 320

Ala Lys Leu Val Gly Tyr Val Ser Ala Gly Thr Val Glu Trp Leu Tyr  
 325 330 335

Ser Pro Glu Ser Gly Glu Phe Ala Phe Leu Glu Leu Asn Pro Arg Leu  
 340 345 350

Gln Val Glu His Pro Thr Thr Glu Met Val Ser Gly Val Asn Ile Pro  
 355 360 365

Ala Ala Gln Leu Gln Val Ala Met Gly Ile Pro Leu Tyr Ser Ile Arg  
 370 375 380

Asp Ile Arg Thr Leu Tyr Gly Met Asp Pro Arg Gly Asn Glu Val Ile  
 385 390 395 400

Asp Phe Asp Phe Ser Ser Pro Glu Ser Phe Lys Thr Gln Arg Lys Pro  
 405 410 415

Gln Pro Gln Gly His Val Val Ala Cys Arg Ile Thr Ala Glu Asn Pro

420                      425                      430  
 Asp Thr Gly Phe Lys Pro Gly Met Gly Ala Leu Thr Glu Leu Asn Phe  
           435                      440                      445  
 Arg Ser Ser Thr Ser Thr Trp Gly Tyr Phe Ser Val Gly Thr Ser Gly  
           450                      455                      460  
 Ala Leu His Glu Tyr Ala Asp Ser Gln Phe Gly His Ile Phe Ala Tyr  
           465                      470                      475                      480  
 Gly Ala Asp Arg Ser Glu Ala Arg Lys Gln Met Val Ile Ser Leu Lys  
                           485                      490                      495  
 Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile  
                           500                      505                      510  
 Lys Leu Leu Glu Thr Asp Ala Phe Glu Ser Asn Lys Ile Thr Thr Gly  
                           515                      520                      525  
 Trp Leu Asp Gly Leu Ile Gln Asp Arg Leu Thr  
           530                      535  
  
 <210> 30  
 <211> 529  
 <212> PRT  
 <213> Ustilago maydis  
  
 <220>  
 <221> MISC\_FEATURE  
 <222> (1)..(529)  
 <223> N- and C-terminal deleted Ustilago ACCase BC domain (AAs 17-545)  
  
 <400> 30  
 Pro Leu Glu Thr Ala Pro Ala Ser Pro Val Ala Asp Phe Ile Arg Lys  
   1                      5                      10                      15  
 Gln Gly Gly His Ser Val Ile Thr Lys Val Leu Ile Cys Asn Asn Gly  
           20                      25                      30  
 Ile Ala Ala Val Lys Glu Ile Arg Ser Ile Arg Lys Trp Ala Tyr Glu  
           35                      40                      45  
 Thr Phe Gly Asp Glu Arg Ala Ile Glu Phe Thr Val Met Ala Thr Pro  
           50                      55                      60  
 Glu Asp Leu Lys Val Asn Ala Asp Tyr Ile Arg Met Ala Asp Gln Tyr

65		70		75		80									
Val	Glu	Val	Pro	Gly	Gly	Ser	Asn	Asn	Asn	Asn	Tyr	Ala	Asn	Val	Asp
				85					90					95	
Leu	Ile	Val	Asp	Val	Ala	Glu	Arg	Ala	Gly	Val	His	Ala	Val	Trp	Ala
			100					105					110		
Gly	Trp	Gly	His	Ala	Ser	Glu	Asn	Pro	Arg	Leu	Pro	Glu	Ser	Leu	Ala
		115					120					125			
Ala	Ser	Lys	His	Lys	Ile	Ile	Phe	Ile	Gly	Pro	Pro	Gly	Ser	Ala	Met
		130					135					140			
Arg	Ser	Leu	Gly	Asp	Lys	Ile	Ser	Ser	Thr	Ile	Val	Ala	Gln	His	Ala
					150					155					160
Asp	Val	Pro	Cys	Met	Pro	Trp	Ser	Gly	Thr	Gly	Ile	Lys	Glu	Thr	Met
				165					170					175	
Met	Ser	Asp	Gln	Gly	Phe	Leu	Thr	Val	Ser	Asp	Asp	Val	Tyr	Gln	Gln
			180					185					190		
Ala	Cys	Ile	His	Thr	Ala	Glu	Glu	Gly	Leu	Glu	Lys	Ala	Glu	Lys	Ile
		195					200					205			
Gly	Tyr	Pro	Val	Met	Ile	Lys	Ala	Ser	Glu	Gly	Gly	Gly	Gly	Lys	Gly
		210				215					220				
Ile	Arg	Lys	Cys	Thr	Asn	Gly	Glu	Glu	Phe	Lys	Gln	Leu	Tyr	Asn	Ala
					230					235					240
Val	Leu	Gly	Glu	Val	Pro	Gly	Ser	Pro	Val	Phe	Val	Met	Lys	Leu	Ala
				245					250					255	
Gly	Gln	Ala	Arg	His	Leu	Glu	Val	Gln	Leu	Leu	Ala	Asp	Gln	Tyr	Gly
			260					265					270		
Asn	Ala	Ile	Ser	Ile	Phe	Gly	Arg	Asp	Cys	Ser	Val	Gln	Arg	Arg	His
		275					280					285			
Gln	Lys	Ile	Ile	Glu	Glu	Ala	Pro	Val	Thr	Ile	Ala	Pro	Glu	Asp	Ala
		290				295					300				
Arg	Glu	Ser	Met	Glu	Lys	Ala	Ala	Val	Arg	Leu	Ala	Lys	Leu	Val	Gly
					310					315					320

Tyr Val Ser Ala Gly Thr Val Glu Trp Leu Tyr Ser Pro Glu Ser Gly  
325 330 335

Glu Phe Ala Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro  
340 345 350

Thr Thr Glu Met Val Ser Gly Val Asn Ile Pro Ala Ala Gln Leu Gln  
355 360 365

Val Ala Met Gly Ile Pro Leu Tyr Ser Ile Arg Asp Ile Arg Thr Leu  
370 375 380

Tyr Gly Met Asp Pro Arg Gly Asn Glu Val Ile Asp Phe Asp Phe Ser  
385 390 395 400

Ser Pro Glu Ser Phe Lys Thr Gln Arg Lys Pro Gln Pro Gln Gly His  
405 410 415

Val Val Ala Cys Arg Ile Thr Ala Glu Asn Pro Asp Thr Gly Phe Lys  
420 425 430

Pro Gly Met Gly Ala Leu Thr Glu Leu Asn Phe Arg Ser Ser Thr Ser  
435 440 445

Thr Trp Gly Tyr Phe Ser Val Gly Thr Ser Gly Ala Leu His Glu Tyr  
450 455 460

Ala Asp Ser Gln Phe Gly His Ile Phe Ala Tyr Gly Ala Asp Arg Ser  
465 470 475 480

Glu Ala Arg Lys Gln Met Val Ile Ser Leu Lys Glu Leu Ser Ile Arg  
485 490 495

Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr  
500 505 510

Asp Ala Phe Glu Ser Asn Lys Ile Thr Thr Gly Trp Leu Asp Gly Leu  
515 520 525

Ile

<210> 31  
<211> 519  
<212> PRT

<213> Ustilago maydis

<220>

<221> MISC\_FEATURE

<222> (1)..(519)

<223> N- and C-terminal deleted Ustilago ACCase BC domain (AAs 22-540)

<400> 31

Pro Ala Ser Pro Val Ala Asp Phe Ile Arg Lys Gln Gly Gly His Ser  
1 5 10 15

Val Ile Thr Lys Val Leu Ile Cys Asn Asn Gly Ile Ala Ala Val Lys  
20 25 30

Glu Ile Arg Ser Ile Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu  
35 40 45

Arg Ala Ile Glu Phe Thr Val Met Ala Thr Pro Glu Asp Leu Lys Val  
50 55 60

Asn Ala Asp Tyr Ile Arg Met Ala Asp Gln Tyr Val Glu Val Pro Gly  
65 70 75 80

Gly Ser Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile Val Asp Val  
85 90 95

Ala Glu Arg Ala Gly Val His Ala Val Trp Ala Gly Trp Gly His Ala  
100 105 110

Ser Glu Asn Pro Arg Leu Pro Glu Ser Leu Ala Ala Ser Lys His Lys  
115 120 125

Ile Ile Phe Ile Gly Pro Pro Gly Ser Ala Met Arg Ser Leu Gly Asp  
130 135 140

Lys Ile Ser Ser Thr Ile Val Ala Gln His Ala Asp Val Pro Cys Met  
145 150 155 160

Pro Trp Ser Gly Thr Gly Ile Lys Glu Thr Met Met Ser Asp Gln Gly  
165 170 175

Phe Leu Thr Val Ser Asp Asp Val Tyr Gln Gln Ala Cys Ile His Thr  
180 185 190

Ala Glu Glu Gly Leu Glu Lys Ala Glu Lys Ile Gly Tyr Pro Val Met  
195 200 205

Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Lys Cys Thr  
 210 215 220

Asn Gly Glu Glu Phe Lys Gln Leu Tyr Asn Ala Val Leu Gly Glu Val  
 225 230 235 240

Pro Gly Ser Pro Val Phe Val Met Lys Leu Ala Gly Gln Ala Arg His  
 245 250 255

Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn Ala Ile Ser Ile  
 260 265 270

Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile Ile Glu  
 275 280 285

Glu Ala Pro Val Thr Ile Ala Pro Glu Asp Ala Arg Glu Ser Met Glu  
 290 295 300

Lys Ala Ala Val Arg Leu Ala Lys Leu Val Gly Tyr Val Ser Ala Gly  
 305 310 315 320

Thr Val Glu Trp Leu Tyr Ser Pro Glu Ser Gly Glu Phe Ala Phe Leu  
 325 330 335

Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr Thr Glu Met Val  
 340 345 350

Ser Gly Val Asn Ile Pro Ala Ala Gln Leu Gln Val Ala Met Gly Ile  
 355 360 365

Pro Leu Tyr Ser Ile Arg Asp Ile Arg Thr Leu Tyr Gly Met Asp Pro  
 370 375 380

Arg Gly Asn Glu Val Ile Asp Phe Asp Phe Ser Ser Pro Glu Ser Phe  
 385 390 395 400

Lys Thr Gln Arg Lys Pro Gln Pro Gln Gly His Val Val Ala Cys Arg  
 405 410 415

Ile Thr Ala Glu Asn Pro Asp Thr Gly Phe Lys Pro Gly Met Gly Ala  
 420 425 430

Leu Thr Glu Leu Asn Phe Arg Ser Ser Thr Ser Thr Trp Gly Tyr Phe  
 435 440 445

Ser Val Gly Thr Ser Gly Ala Leu His Glu Tyr Ala Asp Ser Gln Phe  
 450 455 460

Gly His Ile Phe Ala Tyr Gly Ala Asp Arg Ser Glu Ala Arg Lys Gln  
 465 470 475 480

Met Val Ile Ser Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr  
 485 490 495

Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Asp Ala Phe Glu Ser  
 500 505 510

Asn Lys Ile Thr Thr Gly Trp  
 515

<210> 32  
 <211> 580  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<220>  
 <221> MISC\_FEATURE  
 <222> (76)..(76)  
 <223> *Saccharomyces cerevisiae* ACCase BC domain S77Y mutation

<400> 32

Ser Glu Glu Ser Leu Phe Glu Ser Ser Pro Gln Lys Met Glu Tyr Glu  
 1 5 10 15

Ile Thr Asn Tyr Ser Glu Arg His Thr Glu Leu Pro Gly His Phe Ile  
 20 25 30

Gly Leu Asn Thr Val Asp Lys Leu Glu Glu Ser Pro Leu Arg Asp Phe  
 35 40 45

Val Lys Ser His Gly Gly His Thr Val Ile Ser Lys Ile Leu Ile Ala  
 50 55 60

Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Tyr Val Arg Lys Trp  
 65 70 75 80

Ala Tyr Glu Thr Phe Gly Asp Asp Arg Thr Val Gln Phe Val Ala Met  
 85 90 95

Ala Thr Pro Glu Asp Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met Ala  
 100 105 110



Asp Gln Tyr Ile Glu Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala  
 115 120 125

Asn Val Asp Leu Ile Val Asp Ile Ala Glu Arg Ala Asp Val Asp Ala  
 130 135 140

Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro Glu  
 145 150 155 160

Lys Leu Ser Gln Ser Lys Arg Lys Val Ile Phe Ile Gly Pro Pro Gly  
 165 170 175

Asn Ala Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala  
 180 185 190

Gln Ser Ala Lys Val Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp  
 195 200 205

Thr Val His Val Asp Glu Lys Thr Gly Leu Val Ser Val Asp Asp Asp  
 210 215 220

Ile Tyr Gln Lys Gly Cys Cys Thr Ser Pro Glu Asp Gly Leu Gln Lys  
 225 230 235 240

Ala Lys Arg Ile Gly Phe Pro Val Met Ile Lys Ala Ser Glu Gly Gly  
 245 250 255

Gly Gly Lys Gly Ile Arg Gln Val Glu Arg Glu Glu Asp Phe Ile Ala  
 260 265 270

Leu Tyr His Gln Ala Ala Asn Glu Ile Pro Gly Ser Pro Ile Phe Ile  
 275 280 285

Met Lys Leu Ala Gly Arg Ala Arg His Leu Glu Val Gln Leu Leu Ala  
 290 295 300

Asp Gln Tyr Gly Thr Asn Ile Ser Leu Phe Gly Arg Asp Cys Ser Val  
 305 310 315 320

Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala  
 325 330 335

Lys Ala Glu Thr Phe His Glu Met Glu Lys Ala Ala Val Arg Leu Gly  
 340 345 350

Lys Leu Val Gly Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser

355		360		365
His Asp Asp Gly Lys Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln				
370		375		380
Val Glu His Pro Thr Thr Glu Met Val Ser Gly Val Asn Leu Pro Ala				
385		390		395 400
Ala Gln Leu Gln Ile Ala Met Gly Ile Pro Met His Arg Ile Ser Asp				
	405		410	415
Ile Arg Thr Leu Tyr Gly Met Asn Pro His Ser Ala Ser Glu Ile Asp				
	420		425	430
Phe Glu Phe Lys Thr Gln Asp Ala Thr Lys Lys Gln Arg Arg Pro Ile				
	435		440	445
Pro Lys Gly His Cys Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Asn				
	450		455	460
Asp Gly Phe Lys Pro Ser Gly Gly Thr Leu His Glu Leu Asn Phe Arg				
465		470		475 480
Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly Asn				
	485		490	495
Ile His Ser Phe Ser Asp Ser Gln Phe Gly His Ile Phe Ala Phe Gly				
	500		505	510
Glu Asn Arg Gln Ala Ser Arg Lys His Met Val Val Ala Leu Lys Glu				
	515		520	525
Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys				
	530		535	540
Leu Leu Glu Thr Glu Asp Phe Glu Asp Asn Thr Ile Thr Thr Gly Trp				
545		550		555 560
Leu Asp Asp Leu Ile Thr His Lys Met Thr Ala Glu Lys Pro Asp Pro				
	565		570	575
Thr Leu Ala Val				
	580			

<210> 33  
 <211> 575

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<212>  PRT
<213>  Saccharomyces cerevisiae

<220>
<221>  MISC_FEATURE
<222>  (1)..(575)
<223>  N-terminal deleted Saccharomyces cerevisiae ACCase BC domain (AAs
      7-581)

<400>  33

Phe Glu Ser Ser Pro Gln Lys Met Glu Tyr Glu Ile Thr Asn Tyr Ser
1          5          10          15

Glu Arg His Thr Glu Leu Pro Gly His Phe Ile Gly Leu Asn Thr Val
      20          25          30

Asp Lys Leu Glu Glu Ser Pro Leu Arg Asp Phe Val Lys Ser His Gly
      35          40          45

Gly His Thr Val Ile Ser Lys Ile Leu Ile Ala Asn Asn Gly Ile Ala
      50          55          60

Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe
65          70          75          80

Gly Asp Asp Arg Thr Val Gln Phe Val Ala Met Ala Thr Pro Glu Asp
      85          90          95

Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met Ala Asp Gln Tyr Ile Glu
      100         105         110

Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile
      115         120         125

Val Asp Ile Ala Glu Arg Ala Asp Val Asp Ala Val Trp Ala Gly Trp
      130         135         140

Gly His Ala Ser Glu Asn Pro Leu Leu Pro Glu Lys Leu Ser Gln Ser
145          150          155          160

Lys Arg Lys Val Ile Phe Ile Gly Pro Pro Gly Asn Ala Met Arg Ser
      165         170         175

Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln Ser Ala Lys Val
      180         185         190

Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp Thr Val His Val Asp

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84

Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Asn Asp Gly Phe Lys Pro  
 450 455 460

Ser Gly Gly Thr Leu His Glu Leu Asn Phe Arg Ser Ser Ser Asn Val  
 465 470 475 480

Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly Asn Ile His Ser Phe Ser  
 485 490 495

Asp Ser Gln Phe Gly His Ile Phe Ala Phe Gly Glu Asn Arg Gln Ala  
 500 505 510

Ser Arg Lys His Met Val Val Ala Leu Lys Glu Leu Ser Ile Arg Gly  
 515 520 525

Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu  
 530 535 540

Asp Phe Glu Asp Asn Thr Ile Thr Thr Gly Trp Leu Asp Asp Leu Ile  
 545 550 555 560

Thr His Lys Met Thr Ala Glu Lys Pro Asp Pro Thr Leu Ala Val  
 565 570 575

<210> 34  
 <211> 570  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<220>  
 <221> MISC\_FEATURE  
 <222> (1)..(570)  
 <223> N-terminal deleted *Saccharomyces cerevisiae* ACCase BC domain (AAs  
 12-581)

<400> 34

Gln Lys Met Glu Tyr Glu Ile Thr Asn Tyr Ser Glu Arg His Thr Glu  
 1 5 10 15

Leu Pro Gly His Phe Ile Gly Leu Asn Thr Val Asp Lys Leu Glu Glu  
 20 25 30

Ser Pro Leu Arg Asp Phe Val Lys Ser His Gly Gly His Thr Val Ile  
 35 40 45

Ser Lys Ile Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys Glu Ile

50	55	60																	
Arg	Ser	Val	Arg	Lys	Trp	Ala	Tyr	Glu	Thr	Phe	Gly	Asp	Asp	Arg	Thr				
65					70					75					80				
Val	Gln	Phe	Val	Ala	Met	Ala	Thr	Pro	Glu	Asp	Leu	Glu	Ala	Asn	Ala				
				85					90					95					
Glu	Tyr	Ile	Arg	Met	Ala	Asp	Gln	Tyr	Ile	Glu	Val	Pro	Gly	Gly	Thr				
			100					105					110						
Asn	Asn	Asn	Asn	Tyr	Ala	Asn	Val	Asp	Leu	Ile	Val	Asp	Ile	Ala	Glu				
			115				120					125							
Arg	Ala	Asp	Val	Asp	Ala	Val	Trp	Ala	Gly	Trp	Gly	His	Ala	Ser	Glu				
	130					135					140								
Asn	Pro	Leu	Leu	Pro	Glu	Lys	Leu	Ser	Gln	Ser	Lys	Arg	Lys	Val	Ile				
145					150					155					160				
Phe	Ile	Gly	Pro	Pro	Gly	Asn	Ala	Met	Arg	Ser	Leu	Gly	Asp	Lys	Ile				
				165					170					175					
Ser	Ser	Thr	Ile	Val	Ala	Gln	Ser	Ala	Lys	Val	Pro	Cys	Ile	Pro	Trp				
			180					185					190						
Ser	Gly	Thr	Gly	Val	Asp	Thr	Val	His	Val	Asp	Glu	Lys	Thr	Gly	Leu				
		195					200					205							
Val	Ser	Val	Asp	Asp	Asp	Ile	Tyr	Gln	Lys	Gly	Cys	Cys	Thr	Ser	Pro				
	210					215					220								
Glu	Asp	Gly	Leu	Gln	Lys	Ala	Lys	Arg	Ile	Gly	Phe	Pro	Val	Met	Ile				
225					230					235					240				
Lys	Ala	Ser	Glu	Gly	Gly	Gly	Gly	Lys	Gly	Ile	Arg	Gln	Val	Glu	Arg				
				245					250					255					
Glu	Glu	Asp	Phe	Ile	Ala	Leu	Tyr	His	Gln	Ala	Ala	Asn	Glu	Ile	Pro				
			260					265					270						
Gly	Ser	Pro	Ile	Phe	Ile	Met	Lys	Leu	Ala	Gly	Arg	Ala	Arg	His	Leu				
		275					280					285							
Glu	Val	Gln	Leu	Leu	Ala	Asp	Gln	Tyr	Gly	Thr	Asn	Ile	Ser	Leu	Phe				
	290					295					300								

Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile Ile Glu Glu  
 305 310 315 320

Ala Pro Val Thr Ile Ala Lys Ala Glu Thr Phe His Glu Met Glu Lys  
 325 330 335

Ala Ala Val Arg Leu Gly Lys Leu Val Gly Tyr Val Ser Ala Gly Thr  
 340 345 350

Val Glu Tyr Leu Tyr Ser His Asp Asp Gly Lys Phe Tyr Phe Leu Glu  
 355 360 365

Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr Thr Glu Met Val Ser  
 370 375 380

Gly Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala Met Gly Ile Pro  
 385 390 395 400

Met His Arg Ile Ser Asp Ile Arg Thr Leu Tyr Gly Met Asn Pro His  
 405 410 415

Ser Ala Ser Glu Ile Asp Phe Glu Phe Lys Thr Gln Asp Ala Thr Lys  
 420 425 430

Lys Gln Arg Arg Pro Ile Pro Lys Gly His Cys Thr Ala Cys Arg Ile  
 435 440 445

Thr Ser Glu Asp Pro Asn Asp Gly Phe Lys Pro Ser Gly Gly Thr Leu  
 450 455 460

His Glu Leu Asn Phe Arg Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser  
 465 470 475 480

Val Gly Asn Asn Gly Asn Ile His Ser Phe Ser Asp Ser Gln Phe Gly  
 485 490 495

His Ile Phe Ala Phe Gly Glu Asn Arg Gln Ala Ser Arg Lys His Met  
 500 505 510

Val Val Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr  
 515 520 525

Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Asp Phe Glu Asp Asn  
 530 535 540

Thr Ile Thr Thr Gly Trp Leu Asp Asp Leu Ile Thr His Lys Met Thr  
 545 550 555 560

Ala Glu Lys Pro Asp Pro Thr Leu Ala Val  
 565 570

<210> 35  
 <211> 560  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<220>  
 <221> MISC\_FEATURE  
 <222> (1)..(560)  
 <223> N-terminal deleted *Saccharomyces cerevisiae* ACCase BC domain (AAs  
 22-581)

<400> 35

Ser Glu Arg His Thr Glu Leu Pro Gly His Phe Ile Gly Leu Asn Thr  
 1 5 10 15

Val Asp Lys Leu Glu Glu Ser Pro Leu Arg Asp Phe Val Lys Ser His  
 20 25 30

Gly Gly His Thr Val Ile Ser Lys Ile Leu Ile Ala Asn Asn Gly Ile  
 35 40 45

Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr  
 50 55 60

Phe Gly Asp Asp Arg Thr Val Gln Phe Val Ala Met Ala Thr Pro Glu  
 65 70 75 80

Asp Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met Ala Asp Gln Tyr Ile  
 85 90 95

Glu Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu  
 100 105 110

Ile Val Asp Ile Ala Glu Arg Ala Asp Val Asp Ala Val Trp Ala Gly  
 115 120 125

Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro Glu Lys Leu Ser Gln  
 130 135 140

Ser Lys Arg Lys Val Ile Phe Ile Gly Pro Pro Gly Asn Ala Met Arg  
 145 150 155 160



Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln Ser Ala Lys  
 165 170 175

Val Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp Thr Val His Val  
 180 185 190

Asp Glu Lys Thr Gly Leu Val Ser Val Asp Asp Asp Ile Tyr Gln Lys  
 195 200 205

Gly Cys Cys Thr Ser Pro Glu Asp Gly Leu Gln Lys Ala Lys Arg Ile  
 210 215 220

Gly Phe Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly  
 225 230 235 240

Ile Arg Gln Val Glu Arg Glu Glu Asp Phe Ile Ala Leu Tyr His Gln  
 245 250 255

Ala Ala Asn Glu Ile Pro Gly Ser Pro Ile Phe Ile Met Lys Leu Ala  
 260 265 270

Gly Arg Ala Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly  
 275 280 285

Thr Asn Ile Ser Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His  
 290 295 300

Gln Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala Lys Ala Glu Thr  
 305 310 315 320

Phe His Glu Met Glu Lys Ala Ala Val Arg Leu Gly Lys Leu Val Gly  
 325 330 335

Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser His Asp Asp Gly  
 340 345 350

Lys Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro  
 355 360 365

Thr Thr Glu Met Val Ser Gly Val Asn Leu Pro Ala Ala Gln Leu Gln  
 370 375 380

Ile Ala Met Gly Ile Pro Met His Arg Ile Ser Asp Ile Arg Thr Leu  
 385 390 395 400

Tyr Gly Met Asn Pro His Ser Ala Ser Glu Ile Asp Phe Glu Phe Lys  
405 410 415

Thr Gln Asp Ala Thr Lys Lys Gln Arg Arg Pro Ile Pro Lys Gly His  
420 425 430

Cys Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Asn Asp Gly Phe Lys  
435 440 445

Pro Ser Gly Gly Thr Leu His Glu Leu Asn Phe Arg Ser Ser Ser Asn  
450 455 460

Val Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly Asn Ile His Ser Phe  
465 470 475 480

Ser Asp Ser Gln Phe Gly His Ile Phe Ala Phe Gly Glu Asn Arg Gln  
485 490 495

Ala Ser Arg Lys His Met Val Val Ala Leu Lys Glu Leu Ser Ile Arg  
500 505 510

Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr  
515 520 525

Glu Asp Phe Glu Asp Asn Thr Ile Thr Thr Gly Trp Leu Asp Asp Leu  
530 535 540

Ile Thr His Lys Met Thr Ala Glu Lys Pro Asp Pro Thr Leu Ala Val  
545 550 555 560

<210> 36  
<211> 550  
<212> PRT  
<213> Saccharomyces cerevisiae

<220>  
<221> MISC\_FEATURE  
<222> (1)..(550)  
<223> N-terminal deleted Saccharomyces cerevisiae ACCase BC domain (AAs  
32-581

<400> 36

Phe Ile Gly Leu Asn Thr Val Asp Lys Leu Glu Glu Ser Pro Leu Arg  
1 5 10 15

Asp Phe Val Lys Ser His Gly Gly His Thr Val Ile Ser Lys Ile Leu  
20 25 30

Ile Ala Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Val Arg  
 35 40 45

Lys Trp Ala Tyr Glu Thr Phe Gly Asp Asp Arg Thr Val Gln Phe Val  
 50 55 60

Ala Met Ala Thr Pro Glu Asp Leu Glu Ala Asn Ala Glu Tyr Ile Arg  
 65 70 75 80

Met Ala Asp Gln Tyr Ile Glu Val Pro Gly Gly Thr Asn Asn Asn Asn  
 85 90 95

Tyr Ala Asn Val Asp Leu Ile Val Asp Ile Ala Glu Arg Ala Asp Val  
 100 105 110

Asp Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Leu Leu  
 115 120 125

Pro Glu Lys Leu Ser Gln Ser Lys Arg Lys Val Ile Phe Ile Gly Pro  
 130 135 140

Pro Gly Asn Ala Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile  
 145 150 155 160

Val Ala Gln Ser Ala Lys Val Pro Cys Ile Pro Trp Ser Gly Thr Gly  
 165 170 175

Val Asp Thr Val His Val Asp Glu Lys Thr Gly Leu Val Ser Val Asp  
 180 185 190

Asp Asp Ile Tyr Gln Lys Gly Cys Cys Thr Ser Pro Glu Asp Gly Leu  
 195 200 205

Gln Lys Ala Lys Arg Ile Gly Phe Pro Val Met Ile Lys Ala Ser Glu  
 210 215 220

Gly Gly Gly Gly Lys Gly Ile Arg Gln Val Glu Arg Glu Glu Asp Phe  
 225 230 235 240

Ile Ala Leu Tyr His Gln Ala Ala Asn Glu Ile Pro Gly Ser Pro Ile  
 245 250 255

Phe Ile Met Lys Leu Ala Gly Arg Ala Arg His Leu Glu Val Gln Leu  
 260 265 270

Leu Ala Asp Gln Tyr Gly Thr Asn Ile Ser Leu Phe Gly Arg Asp Cys  
 275 280 285

Ser Val Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala Pro Val Thr  
 290 295 300

Ile Ala Lys Ala Glu Thr Phe His Glu Met Glu Lys Ala Ala Val Arg  
 305 310 315 320

Leu Gly Lys Leu Val Gly Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu  
 325 330 335

Tyr Ser His Asp Asp Gly Lys Phe Tyr Phe Leu Glu Leu Asn Pro Arg  
 340 345 350

Leu Gln Val Glu His Pro Thr Thr Glu Met Val Ser Gly Val Asn Leu  
 355 360 365

Pro Ala Ala Gln Leu Gln Ile Ala Met Gly Ile Pro Met His Arg Ile  
 370 375 380

Ser Asp Ile Arg Thr Leu Tyr Gly Met Asn Pro His Ser Ala Ser Glu  
 385 390 395 400

Ile Asp Phe Glu Phe Lys Thr Gln Asp Ala Thr Lys Lys Gln Arg Arg  
 405 410 415

Pro Ile Pro Lys Gly His Cys Thr Ala Cys Arg Ile Thr Ser Glu Asp  
 420 425 430

Pro Asn Asp Gly Phe Lys Pro Ser Gly Gly Thr Leu His Glu Leu Asn  
 435 440 445

Phe Arg Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val Gly Asn Asn  
 450 455 460

Gly Asn Ile His Ser Phe Ser Asp Ser Gln Phe Gly His Ile Phe Ala  
 465 470 475 480

Phe Gly Glu Asn Arg Gln Ala Ser Arg Lys His Met Val Val Ala Leu  
 485 490 495

Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu  
 500 505 510

Ile Lys Leu Leu Glu Thr Glu Asp Phe Glu Asp Asn Thr Ile Thr Thr  
515 520 525

Gly Trp Leu Asp Asp Leu Ile Thr His Lys Met Thr Ala Glu Lys Pro  
530 535 540

Asp Pro Thr Leu Ala Val  
545 550

<210> 37  
<211> 540  
<212> PRT  
<213> Saccharomyces cerevisiae

<220>  
<221> MISC\_FEATURE  
<222> (1)..(540)  
<223> N-terminal deleted Saccharomyces cerevisiae ACCase BC domain (AAs  
42-581)

<400> 37

Glu Glu Ser Pro Leu Arg Asp Phe Val Lys Ser His Gly Gly His Thr  
1 5 10 15

Val Ile Ser Lys Ile Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys  
20 25 30

Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp Asp  
35 40 45

Arg Thr Val Gln Phe Val Ala Met Ala Thr Pro Glu Asp Leu Glu Ala  
50 55 60

Asn Ala Glu Tyr Ile Arg Met Ala Asp Gln Tyr Ile Glu Val Pro Gly  
65 70 75 80

Gly Thr Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile Val Asp Ile  
85 90 95

Ala Glu Arg Ala Asp Val Asp Ala Val Trp Ala Gly Trp Gly His Ala  
100 105 110

Ser Glu Asn Pro Leu Leu Pro Glu Lys Leu Ser Gln Ser Lys Arg Lys  
115 120 125

Val Ile Phe Ile Gly Pro Pro Gly Asn Ala Met Arg Ser Leu Gly Asp  
130 135 140

Lys Ile Ser Ser Thr Ile Val Ala Gln Ser Ala Lys Val Pro Cys Ile  
 145 150 155 160

Pro Trp Ser Gly Thr Gly Val Asp Thr Val His Val Asp Glu Lys Thr  
 165 170 175

Gly Leu Val Ser Val Asp Asp Asp Ile Tyr Gln Lys Gly Cys Cys Thr  
 180 185 190

Ser Pro Glu Asp Gly Leu Gln Lys Ala Lys Arg Ile Gly Phe Pro Val  
 195 200 205

Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Gln Val  
 210 215 220

Glu Arg Glu Glu Asp Phe Ile Ala Leu Tyr His Gln Ala Ala Asn Glu  
 225 230 235 240

Ile Pro Gly Ser Pro Ile Phe Ile Met Lys Leu Ala Gly Arg Ala Arg  
 245 250 255

His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Thr Asn Ile Ser  
 260 265 270

Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile Ile  
 275 280 285

Glu Glu Ala Pro Val Thr Ile Ala Lys Ala Glu Thr Phe His Glu Met  
 290 295 300

Glu Lys Ala Ala Val Arg Leu Gly Lys Leu Val Gly Tyr Val Ser Ala  
 305 310 315 320

Gly Thr Val Glu Tyr Leu Tyr Ser His Asp Asp Gly Lys Phe Tyr Phe  
 325 330 335

Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr Thr Glu Met  
 340 345 350

Val Ser Gly Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala Met Gly  
 355 360 365

Ile Pro Met His Arg Ile Ser Asp Ile Arg Thr Leu Tyr Gly Met Asn  
 370 375 380

Pro His Ser Ala Ser Glu Ile Asp Phe Glu Phe Lys Thr Gln Asp Ala  
385 390 395 400

Thr Lys Lys Gln Arg Arg Pro Ile Pro Lys Gly His Cys Thr Ala Cys  
405 410 415

Arg Ile Thr Ser Glu Asp Pro Asn Asp Gly Phe Lys Pro Ser Gly Gly  
420 425 430

Thr Leu His Glu Leu Asn Phe Arg Ser Ser Ser Asn Val Trp Gly Tyr  
435 440 445

Phe Ser Val Gly Asn Asn Gly Asn Ile His Ser Phe Ser Asp Ser Gln  
450 455 460

Phe Gly His Ile Phe Ala Phe Gly Glu Asn Arg Gln Ala Ser Arg Lys  
465 470 475 480

His Met Val Val Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg  
485 490 495

Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Asp Phe Glu  
500 505 510

Asp Asn Thr Ile Thr Thr Gly Trp Leu Asp Asp Leu Ile Thr His Lys  
515 520 525

Met Thr Ala Glu Lys Pro Asp Pro Thr Leu Ala Val  
530 535 540

<210> 38  
<211> 575  
<212> PRT  
<213> Saccharomyces cerevisiae

<220>  
<221> MISC\_FEATURE  
<222> (1)..(575)  
<223> C-terminal deleted Saccharomyces cerevisiae ACCase BC domain (AAs  
2-576)

<400> 38

Ser Glu Glu Ser Leu Phe Glu Ser Ser Pro Gln Lys Met Glu Tyr Glu  
1 5 10 15

Ile Thr Asn Tyr Ser Glu Arg His Thr Glu Leu Pro Gly His Phe Ile  
20 25 30

Gly Leu Asn Thr Val Asp Lys Leu Glu Glu Ser Pro Leu Arg Asp Phe  
 35 40 45

Val Lys Ser His Gly Gly His Thr Val Ile Ser Lys Ile Leu Ile Ala  
 50 55 60

Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp  
 65 70 75 80

Ala Tyr Glu Thr Phe Gly Asp Asp Arg Thr Val Gln Phe Val Ala Met  
 85 90 95

Ala Thr Pro Glu Asp Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met Ala  
 100 105 110

Asp Gln Tyr Ile Glu Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala  
 115 120 125

Asn Val Asp Leu Ile Val Asp Ile Ala Glu Arg Ala Asp Val Asp Ala  
 130 135 140

Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro Glu  
 145 150 155 160

Lys Leu Ser Gln Ser Lys Arg Lys Val Ile Phe Ile Gly Pro Pro Gly  
 165 170 175

Asn Ala Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala  
 180 185 190

Gln Ser Ala Lys Val Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp  
 195 200 205

Thr Val His Val Asp Glu Lys Thr Gly Leu Val Ser Val Asp Asp Asp  
 210 215 220

Ile Tyr Gln Lys Gly Cys Cys Thr Ser Pro Glu Asp Gly Leu Gln Lys  
 225 230 235 240

Ala Lys Arg Ile Gly Phe Pro Val Met Ile Lys Ala Ser Glu Gly Gly  
 245 250 255

Gly Gly Lys Gly Ile Arg Gln Val Glu Arg Glu Glu Asp Phe Ile Ala  
 260 265 270



Leu Tyr His Gln Ala Ala Asn Glu Ile Pro Gly Ser Pro Ile Phe Ile  
 275 280 285

Met Lys Leu Ala Gly Arg Ala Arg His Leu Glu Val Gln Leu Leu Ala  
 290 295 300

Asp Gln Tyr Gly Thr Asn Ile Ser Leu Phe Gly Arg Asp Cys Ser Val  
 305 310 315 320

Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala  
 325 330 335

Lys Ala Glu Thr Phe His Glu Met Glu Lys Ala Ala Val Arg Leu Gly  
 340 345 350

Lys Leu Val Gly Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser  
 355 360 365

His Asp Asp Gly Lys Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln  
 370 375 380

Val Glu His Pro Thr Thr Glu Met Val Ser Gly Val Asn Leu Pro Ala  
 385 390 395 400

Ala Gln Leu Gln Ile Ala Met Gly Ile Pro Met His Arg Ile Ser Asp  
 405 410 415

Ile Arg Thr Leu Tyr Gly Met Asn Pro His Ser Ala Ser Glu Ile Asp  
 420 425 430

Phe Glu Phe Lys Thr Gln Asp Ala Thr Lys Lys Gln Arg Arg Pro Ile  
 435 440 445

Pro Lys Gly His Cys Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Asn  
 450 455 460

Asp Gly Phe Lys Pro Ser Gly Gly Thr Leu His Glu Leu Asn Phe Arg  
 465 470 475 480

Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly Asn  
 485 490 495

Ile His Ser Phe Ser Asp Ser Gln Phe Gly His Ile Phe Ala Phe Gly  
 500 505 510

Glu Asn Arg Gln Ala Ser Arg Lys His Met Val Val Ala Leu Lys Glu

515                      520                      525  
 Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys  
     530                      535                      540  
  
 Leu Leu Glu Thr Glu Asp Phe Glu Asp Asn Thr Ile Thr Thr Gly Trp  
 545                      550                      555                      560  
  
 Leu Asp Asp Leu Ile Thr His Lys Met Thr Ala Glu Lys Pro Asp  
                     565                      570                      575  
  
 <210> 39  
 <211> 570  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*  
  
 <220>  
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 <222> (1)..(570)  
 <223> C-terminal deleted *Saccharomyces cerevisiae* ACCase BC domain (AAs  
                     2-571)  
  
 <400> 39  
  
 Ser Glu Glu Ser Leu Phe Glu Ser Ser Pro Gln Lys Met Glu Tyr Glu  
 1                      5                      10                      15  
  
 Ile Thr Asn Tyr Ser Glu Arg His Thr Glu Leu Pro Gly His Phe Ile  
                     20                      25                      30  
  
 Gly Leu Asn Thr Val Asp Lys Leu Glu Glu Ser Pro Leu Arg Asp Phe  
                     35                      40                      45  
  
 Val Lys Ser His Gly Gly His Thr Val Ile Ser Lys Ile Leu Ile Ala  
                     50                      55                      60  
  
 Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp  
 65                      70                      75                      80  
  
 Ala Tyr Glu Thr Phe Gly Asp Asp Arg Thr Val Gln Phe Val Ala Met  
                     85                      90                      95  
  
 Ala Thr Pro Glu Asp Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met Ala  
                     100                      105                      110  
  
 Asp Gln Tyr Ile Glu Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala  
                     115                      120                      125

Asn Val Asp Leu Ile Val Asp Ile Ala Glu Arg Ala Asp Val Asp Ala  
 130 135 140

Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro Glu  
 145 150 155 160

Lys Leu Ser Gln Ser Lys Arg Lys Val Ile Phe Ile Gly Pro Pro Gly  
 165 170 175

Asn Ala Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala  
 180 185 190

Gln Ser Ala Lys Val Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp  
 195 200 205

Thr Val His Val Asp Glu Lys Thr Gly Leu Val Ser Val Asp Asp Asp  
 210 215 220

Ile Tyr Gln Lys Gly Cys Cys Thr Ser Pro Glu Asp Gly Leu Gln Lys  
 225 230 235 240

Ala Lys Arg Ile Gly Phe Pro Val Met Ile Lys Ala Ser Glu Gly Gly  
 245 250 255

Gly Gly Lys Gly Ile Arg Gln Val Glu Arg Glu Glu Asp Phe Ile Ala  
 260 265 270

Leu Tyr His Gln Ala Ala Asn Glu Ile Pro Gly Ser Pro Ile Phe Ile  
 275 280 285

Met Lys Leu Ala Gly Arg Ala Arg His Leu Glu Val Gln Leu Leu Ala  
 290 295 300

Asp Gln Tyr Gly Thr Asn Ile Ser Leu Phe Gly Arg Asp Cys Ser Val  
 305 310 315 320

Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala  
 325 330 335

Lys Ala Glu Thr Phe His Glu Met Glu Lys Ala Ala Val Arg Leu Gly  
 340 345 350

Lys Leu Val Gly Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser  
 355 360 365

His Asp Asp Gly Lys Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln

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370              375              380

Val Glu His Pro Thr Thr Glu Met Val Ser Gly Val Asn Leu Pro Ala
385              390              395              400

Ala Gln Leu Gln Ile Ala Met Gly Ile Pro Met His Arg Ile Ser Asp
              405              410              415

Ile Arg Thr Leu Tyr Gly Met Asn Pro His Ser Ala Ser Glu Ile Asp
              420              425              430

Phe Glu Phe Lys Thr Gln Asp Ala Thr Lys Lys Gln Arg Arg Pro Ile
              435              440              445

Pro Lys Gly His Cys Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Asn
              450              455              460

Asp Gly Phe Lys Pro Ser Gly Gly Thr Leu His Glu Leu Asn Phe Arg
465              470              475              480

Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly Asn
              485              490              495

Ile His Ser Phe Ser Asp Ser Gln Phe Gly His Ile Phe Ala Phe Gly
              500              505              510

Glu Asn Arg Gln Ala Ser Arg Lys His Met Val Val Ala Leu Lys Glu
              515              520              525

Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys
              530              535              540

Leu Leu Glu Thr Glu Asp Phe Glu Asp Asn Thr Ile Thr Thr Gly Trp
545              550              555              560

Leu Asp Asp Leu Ile Thr His Lys Met Thr
              565              570

<210>  40
<211>  560
<212>  PRT
<213>  Saccharomyces cerevisiae

<220>
<221>  MISC_FEATURE
<222>  (1)..(560)
<223>  C-terminal deleted Saccharomyces cerevisiae ACCase BC domain (AAs

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2-561)

<400> 40

Ser Glu Glu Ser Leu Phe Glu Ser Ser Pro Gln Lys Met Glu Tyr Glu  
1 5 10 15

Ile Thr Asn Tyr Ser Glu Arg His Thr Glu Leu Pro Gly His Phe Ile  
20 25 30

Gly Leu Asn Thr Val Asp Lys Leu Glu Glu Ser Pro Leu Arg Asp Phe  
35 40 45

Val Lys Ser His Gly Gly His Thr Val Ile Ser Lys Ile Leu Ile Ala  
50 55 60

Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp  
65 70 75 80

Ala Tyr Glu Thr Phe Gly Asp Asp Arg Thr Val Gln Phe Val Ala Met  
85 90 95

Ala Thr Pro Glu Asp Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met Ala  
100 105 110

Asp Gln Tyr Ile Glu Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala  
115 120 125

Asn Val Asp Leu Ile Val Asp Ile Ala Glu Arg Ala Asp Val Asp Ala  
130 135 140

Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro Glu  
145 150 155 160

Lys Leu Ser Gln Ser Lys Arg Lys Val Ile Phe Ile Gly Pro Pro Gly  
165 170 175

Asn Ala Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala  
180 185 190

Gln Ser Ala Lys Val Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp  
195 200 205

Thr Val His Val Asp Glu Lys Thr Gly Leu Val Ser Val Asp Asp Asp  
210 215 220

Ile Tyr Gln Lys Gly Cys Cys Thr Ser Pro Glu Asp Gly Leu Gln Lys

225		230		235		240
Ala Lys Arg Ile Gly Phe Pro Val Met Ile Lys Ala Ser Glu Gly Gly						
	245		250		255	
Gly Gly Lys Gly Ile Arg Gln Val Glu Arg Glu Glu Asp Phe Ile Ala						
	260		265		270	
Leu Tyr His Gln Ala Ala Asn Glu Ile Pro Gly Ser Pro Ile Phe Ile						
	275		280		285	
Met Lys Leu Ala Gly Arg Ala Arg His Leu Glu Val Gln Leu Leu Ala						
	290		295		300	
Asp Gln Tyr Gly Thr Asn Ile Ser Leu Phe Gly Arg Asp Cys Ser Val						
305		310		315		320
Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala						
	325		330		335	
Lys Ala Glu Thr Phe His Glu Met Glu Lys Ala Ala Val Arg Leu Gly						
	340		345		350	
Lys Leu Val Gly Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser						
	355		360		365	
His Asp Asp Gly Lys Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln						
	370		375		380	
Val Glu His Pro Thr Thr Glu Met Val Ser Gly Val Asn Leu Pro Ala						
385		390		395		400
Ala Gln Leu Gln Ile Ala Met Gly Ile Pro Met His Arg Ile Ser Asp						
	405		410		415	
Ile Arg Thr Leu Tyr Gly Met Asn Pro His Ser Ala Ser Glu Ile Asp						
	420		425		430	
Phe Glu Phe Lys Thr Gln Asp Ala Thr Lys Lys Gln Arg Arg Pro Ile						
	435		440		445	
Pro Lys Gly His Cys Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Asn						
	450		455		460	
Asp Gly Phe Lys Pro Ser Gly Gly Thr Leu His Glu Leu Asn Phe Arg						
465		470		475		480

Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly Asn  
485 490 495

Ile His Ser Phe Ser Asp Ser Gln Phe Gly His Ile Phe Ala Phe Gly  
500 505 510

Glu Asn Arg Gln Ala Ser Arg Lys His Met Val Val Ala Leu Lys Glu  
515 520 525

Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys  
530 535 540

Leu Leu Glu Thr Glu Asp Phe Glu Asp Asn Thr Ile Thr Thr Gly Trp  
545 550 555 560

<210> 41  
<211> 550  
<212> PRT  
<213> Saccharomyces cerevisiae

<220>  
<221> MISC\_FEATURE  
<222> (1)..(550)  
<223> C-terminal deleted Saccharomyces cerevisiae ACCase BC domain (AAs  
2-551)

<400> 41

Ser Glu Glu Ser Leu Phe Glu Ser Ser Pro Gln Lys Met Glu Tyr Glu  
1 5 10 15

Ile Thr Asn Tyr Ser Glu Arg His Thr Glu Leu Pro Gly His Phe Ile  
20 25 30

Gly Leu Asn Thr Val Asp Lys Leu Glu Glu Ser Pro Leu Arg Asp Phe  
35 40 45

Val Lys Ser His Gly Gly His Thr Val Ile Ser Lys Ile Leu Ile Ala  
50 55 60

Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp  
65 70 75 80

Ala Tyr Glu Thr Phe Gly Asp Asp Arg Thr Val Gln Phe Val Ala Met  
85 90 95

Ala Thr Pro Glu Asp Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met Ala

100	105	110
Asp Gln Tyr Ile Glu Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala 115 120 125		
Asn Val Asp Leu Ile Val Asp Ile Ala Glu Arg Ala Asp Val Asp Ala 130 135 140		
Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro Glu 145 150 155 160		
Lys Leu Ser Gln Ser Lys Arg Lys Val Ile Phe Ile Gly Pro Pro Gly 165 170 175		
Asn Ala Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala 180 185 190		
Gln Ser Ala Lys Val Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp 195 200 205		
Thr Val His Val Asp Glu Lys Thr Gly Leu Val Ser Val Asp Asp Asp 210 215 220		
Ile Tyr Gln Lys Gly Cys Cys Thr Ser Pro Glu Asp Gly Leu Gln Lys 225 230 235 240		
Ala Lys Arg Ile Gly Phe Pro Val Met Ile Lys Ala Ser Glu Gly Gly 245 250 255		
Gly Gly Lys Gly Ile Arg Gln Val Glu Arg Glu Glu Asp Phe Ile Ala 260 265 270		
Leu Tyr His Gln Ala Ala Asn Glu Ile Pro Gly Ser Pro Ile Phe Ile 275 280 285		
Met Lys Leu Ala Gly Arg Ala Arg His Leu Glu Val Gln Leu Leu Ala 290 295 300		
Asp Gln Tyr Gly Thr Asn Ile Ser Leu Phe Gly Arg Asp Cys Ser Val 305 310 315 320		
Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala 325 330 335		
Lys Ala Glu Thr Phe His Glu Met Glu Lys Ala Ala Val Arg Leu Gly 340 345 350		



Lys Leu Val Gly Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser  
 355 360 365

His Asp Asp Gly Lys Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln  
 370 375 380

Val Glu His Pro Thr Thr Glu Met Val Ser Gly Val Asn Leu Pro Ala  
 385 390 395 400

Ala Gln Leu Gln Ile Ala Met Gly Ile Pro Met His Arg Ile Ser Asp  
 405 410 415

Ile Arg Thr Leu Tyr Gly Met Asn Pro His Ser Ala Ser Glu Ile Asp  
 420 425 430

Phe Glu Phe Lys Thr Gln Asp Ala Thr Lys Lys Gln Arg Arg Pro Ile  
 435 440 445

Pro Lys Gly His Cys Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Asn  
 450 455 460

Asp Gly Phe Lys Pro Ser Gly Gly Thr Leu His Glu Leu Asn Phe Arg  
 465 470 475 480

Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly Asn  
 485 490 495

Ile His Ser Phe Ser Asp Ser Gln Phe Gly His Ile Phe Ala Phe Gly  
 500 505 510

Glu Asn Arg Gln Ala Ser Arg Lys His Met Val Val Ala Leu Lys Glu  
 515 520 525

Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys  
 530 535 540

Leu Leu Glu Thr Glu Asp  
 545 550

<210> 42  
 <211> 540  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<220>

<221> MISC\_FEATURE  
 <222> (1)..(540)  
 <223> C-terminal deleted *Saccharomyces cerevisiae* ACCase BC domain (AAs  
 2-541)

<400> 42

Ser Glu Glu Ser Leu Phe Glu Ser Ser Pro Gln Lys Met Glu Tyr Glu  
 1 5 10 15

Ile Thr Asn Tyr Ser Glu Arg His Thr Glu Leu Pro Gly His Phe Ile  
 20 25 30

Gly Leu Asn Thr Val Asp Lys Leu Glu Glu Ser Pro Leu Arg Asp Phe  
 35 40 45

Val Lys Ser His Gly Gly His Thr Val Ile Ser Lys Ile Leu Ile Ala  
 50 55 60

Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp  
 65 70 75 80

Ala Tyr Glu Thr Phe Gly Asp Asp Arg Thr Val Gln Phe Val Ala Met  
 85 90 95

Ala Thr Pro Glu Asp Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met Ala  
 100 105 110

Asp Gln Tyr Ile Glu Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala  
 115 120 125

Asn Val Asp Leu Ile Val Asp Ile Ala Glu Arg Ala Asp Val Asp Ala  
 130 135 140

Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro Glu  
 145 150 155 160

Lys Leu Ser Gln Ser Lys Arg Lys Val Ile Phe Ile Gly Pro Pro Gly  
 165 170 175

Asn Ala Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala  
 180 185 190

Gln Ser Ala Lys Val Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp  
 195 200 205

Thr Val His Val Asp Glu Lys Thr Gly Leu Val Ser Val Asp Asp Asp  
 210 215 220

Ile Tyr Gln Lys Gly Cys Cys Thr Ser Pro Glu Asp Gly Leu Gln Lys  
 225 230 235 240

Ala Lys Arg Ile Gly Phe Pro Val Met Ile Lys Ala Ser Glu Gly Gly  
 245 250 255

Gly Gly Lys Gly Ile Arg Gln Val Glu Arg Glu Glu Asp Phe Ile Ala  
 260 265 270

Leu Tyr His Gln Ala Ala Asn Glu Ile Pro Gly Ser Pro Ile Phe Ile  
 275 280 285

Met Lys Leu Ala Gly Arg Ala Arg His Leu Glu Val Gln Leu Leu Ala  
 290 295 300

Asp Gln Tyr Gly Thr Asn Ile Ser Leu Phe Gly Arg Asp Cys Ser Val  
 305 310 315 320

Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala  
 325 330 335

Lys Ala Glu Thr Phe His Glu Met Glu Lys Ala Ala Val Arg Leu Gly  
 340 345 350

Lys Leu Val Gly Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser  
 355 360 365

His Asp Asp Gly Lys Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln  
 370 375 380

Val Glu His Pro Thr Thr Glu Met Val Ser Gly Val Asn Leu Pro Ala  
 385 390 395 400

Ala Gln Leu Gln Ile Ala Met Gly Ile Pro Met His Arg Ile Ser Asp  
 405 410 415

Ile Arg Thr Leu Tyr Gly Met Asn Pro His Ser Ala Ser Glu Ile Asp  
 420 425 430

Phe Glu Phe Lys Thr Gln Asp Ala Thr Lys Lys Gln Arg Arg Pro Ile  
 435 440 445

Pro Lys Gly His Cys Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Asn  
 450 455 460

Asp Gly Phe Lys Pro Ser Gly Gly Thr Leu His Glu Leu Asn Phe Arg  
 465 470 475 480

Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly Asn  
 485 490 495

Ile His Ser Phe Ser Asp Ser Gln Phe Gly His Ile Phe Ala Phe Gly  
 500 505 510

Glu Asn Arg Gln Ala Ser Arg Lys His Met Val Val Ala Leu Lys Glu  
 515 520 525

Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu  
 530 535 540

<210> 43  
 <211> 575  
 <212> PRT  
 <213> Saccharomyces cerevisiae

<220>  
 <221> MISC\_FEATURE  
 <222> (1)..(575)  
 <223> N- and C-terminal deleted Saccharomyces cerevisiae ACCase BC  
 domain (AAs 4-578)

<400> 43

Glu Ser Leu Phe Glu Ser Ser Pro Gln Lys Met Glu Tyr Glu Ile Thr  
 1 5 10 15

Asn Tyr Ser Glu Arg His Thr Glu Leu Pro Gly His Phe Ile Gly Leu  
 20 25 30

Asn Thr Val Asp Lys Leu Glu Glu Ser Pro Leu Arg Asp Phe Val Lys  
 35 40 45

Ser His Gly Gly His Thr Val Ile Ser Lys Ile Leu Ile Ala Asn Asn  
 50 55 60

Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr  
 65 70 75 80

Glu Thr Phe Gly Asp Asp Arg Thr Val Gln Phe Val Ala Met Ala Thr  
 85 90 95

Pro Glu Asp Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met Ala Asp Gln  
 100 105 110

Tyr Ile Glu Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala Asn Val  
 115 120 125

Asp Leu Ile Val Asp Ile Ala Glu Arg Ala Asp Val Asp Ala Val Trp  
 130 135 140

Ala Gly Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro Glu Lys Leu  
 145 150 155 160

Ser Gln Ser Lys Arg Lys Val Ile Phe Ile Gly Pro Pro Gly Asn Ala  
 165 170 175

Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln Ser  
 180 185 190

Ala Lys Val Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp Thr Val  
 195 200 205

His Val Asp Glu Lys Thr Gly Leu Val Ser Val Asp Asp Asp Ile Tyr  
 210 215 220

Gln Lys Gly Cys Cys Thr Ser Pro Glu Asp Gly Leu Gln Lys Ala Lys  
 225 230 235 240

Arg Ile Gly Phe Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly  
 245 250 255

Lys Gly Ile Arg Gln Val Glu Arg Glu Glu Asp Phe Ile Ala Leu Tyr  
 260 265 270

His Gln Ala Ala Asn Glu Ile Pro Gly Ser Pro Ile Phe Ile Met Lys  
 275 280 285

Leu Ala Gly Arg Ala Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln  
 290 295 300

Tyr Gly Thr Asn Ile Ser Leu Phe Gly Arg Asp Cys Ser Val Gln Arg  
 305 310 315 320

Arg His Gln Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala Lys Ala  
 325 330 335

Glu Thr Phe His Glu Met Glu Lys Ala Ala Val Arg Leu Gly Lys Leu  
 340 345 350

Val Gly Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser His Asp  
355 360 365  
Asp Gly Lys Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu  
370 375 380  
His Pro Thr Thr Glu Met Val Ser Gly Val Asn Leu Pro Ala Ala Gln  
385 390 395 400  
Leu Gln Ile Ala Met Gly Ile Pro Met His Arg Ile Ser Asp Ile Arg  
405 410 415  
Thr Leu Tyr Gly Met Asn Pro His Ser Ala Ser Glu Ile Asp Phe Glu  
420 425 430  
Phe Lys Thr Gln Asp Ala Thr Lys Lys Gln Arg Arg Pro Ile Pro Lys  
435 440 445  
Gly His Cys Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Asn Asp Gly  
450 455 460  
Phe Lys Pro Ser Gly Gly Thr Leu His Glu Leu Asn Phe Arg Ser Ser  
465 470 475 480  
Ser Asn Val Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly Asn Ile His  
485 490 495  
Ser Phe Ser Asp Ser Gln Phe Gly His Ile Phe Ala Phe Gly Glu Asn  
500 505 510  
Arg Gln Ala Ser Arg Lys His Met Val Val Ala Leu Lys Glu Leu Ser  
515 520 525  
Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu  
530 535 540  
Glu Thr Glu Asp Phe Glu Asp Asn Thr Ile Thr Thr Gly Trp Leu Asp  
545 550 555 560  
Asp Leu Ile Thr His Lys Met Thr Ala Glu Lys Pro Asp Pro Thr  
565 570 575

<210> 44  
<211> 570  
<212> PRT  
<213> *Saccharomyces cerevisiae*

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<220>
<221> MISC_FEATURE
<222> (1)..(570)
<223> N- and C-terminal deleted Saccharomyces cerevisiae ACCase BC
        domain (AAs 7-576)

<400> 44

Phe Glu Ser Ser Pro Gln Lys Met Glu Tyr Glu Ile Thr Asn Tyr Ser
1              5              10              15

Glu Arg His Thr Glu Leu Pro Gly His Phe Ile Gly Leu Asn Thr Val
                20              25              30

Asp Lys Leu Glu Glu Ser Pro Leu Arg Asp Phe Val Lys Ser His Gly
        35              40              45

Gly His Thr Val Ile Ser Lys Ile Leu Ile Ala Asn Asn Gly Ile Ala
        50              55              60

Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe
65              70              75              80

Gly Asp Asp Arg Thr Val Gln Phe Val Ala Met Ala Thr Pro Glu Asp
        85              90              95

Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met Ala Asp Gln Tyr Ile Glu
        100             105             110

Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile
        115             120             125

Val Asp Ile Ala Glu Arg Ala Asp Val Asp Ala Val Trp Ala Gly Trp
        130             135             140

Gly His Ala Ser Glu Asn Pro Leu Leu Pro Glu Lys Leu Ser Gln Ser
145             150             155             160

Lys Arg Lys Val Ile Phe Ile Gly Pro Pro Gly Asn Ala Met Arg Ser
        165             170             175

Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln Ser Ala Lys Val
        180             185             190

Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp Thr Val His Val Asp
        195             200             205

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Glu Lys Thr Gly Leu Val Ser Val Asp Asp Asp Ile Tyr Gln Lys Gly  
 210 215 220

Cys Cys Thr Ser Pro Glu Asp Gly Leu Gln Lys Ala Lys Arg Ile Gly  
 225 230 235 240

Phe Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile  
 245 250 255

Arg Gln Val Glu Arg Glu Glu Asp Phe Ile Ala Leu Tyr His Gln Ala  
 260 265 270

Ala Asn Glu Ile Pro Gly Ser Pro Ile Phe Ile Met Lys Leu Ala Gly  
 275 280 285

Arg Ala Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Thr  
 290 295 300

Asn Ile Ser Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln  
 305 310 315 320

Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala Lys Ala Glu Thr Phe  
 325 330 335

His Glu Met Glu Lys Ala Ala Val Arg Leu Gly Lys Leu Val Gly Tyr  
 340 345 350

Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser His Asp Asp Gly Lys  
 355 360 365

Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr  
 370 375 380

Thr Glu Met Val Ser Gly Val Asn Leu Pro Ala Ala Gln Leu Gln Ile  
 385 390 395 400

Ala Met Gly Ile Pro Met His Arg Ile Ser Asp Ile Arg Thr Leu Tyr  
 405 410 415

Gly Met Asn Pro His Ser Ala Ser Glu Ile Asp Phe Glu Phe Lys Thr  
 420 425 430

Gln Asp Ala Thr Lys Lys Gln Arg Arg Pro Ile Pro Lys Gly His Cys  
 435 440 445



Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Asn Asp Gly Phe Lys Pro  
 450 455 460

Ser Gly Gly Thr Leu His Glu Leu Asn Phe Arg Ser Ser Ser Asn Val  
 465 470 475 480

Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly Asn Ile His Ser Phe Ser  
 485 490 495

Asp Ser Gln Phe Gly His Ile Phe Ala Phe Gly Glu Asn Arg Gln Ala  
 500 505 510

Ser Arg Lys His Met Val Val Ala Leu Lys Glu Leu Ser Ile Arg Gly  
 515 520 525

Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu  
 530 535 540

Asp Phe Glu Asp Asn Thr Ile Thr Thr Gly Trp Leu Asp Asp Leu Ile  
 545 550 555 560

Thr His Lys Met Thr Ala Glu Lys Pro Asp  
 565 570

<210> 45  
 <211> 560  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<220>  
 <221> MISC\_FEATURE  
 <222> (1)..(560)  
 <223> N- and C-terminal deleted *Saccharomyces cerevisiae* ACCase BC  
 domain (AAs 12-571)

<400> 45

Gln Lys Met Glu Tyr Glu Ile Thr Asn Tyr Ser Glu Arg His Thr Glu  
 1 5 10 15

Leu Pro Gly His Phe Ile Gly Leu Asn Thr Val Asp Lys Leu Glu Glu  
 20 25 30

Ser Pro Leu Arg Asp Phe Val Lys Ser His Gly Gly His Thr Val Ile  
 35 40 45

Ser Lys Ile Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys Glu Ile  
 50 55 60

Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp Asp Arg Thr  
 65 70 75 80

Val Gln Phe Val Ala Met Ala Thr Pro Glu Asp Leu Glu Ala Asn Ala  
 85 90 95

Glu Tyr Ile Arg Met Ala Asp Gln Tyr Ile Glu Val Pro Gly Gly Thr  
 100 105 110

Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile Val Asp Ile Ala Glu  
 115 120 125

Arg Ala Asp Val Asp Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu  
 130 135 140

Asn Pro Leu Leu Pro Glu Lys Leu Ser Gln Ser Lys Arg Lys Val Ile  
 145 150 155 160

Phe Ile Gly Pro Pro Gly Asn Ala Met Arg Ser Leu Gly Asp Lys Ile  
 165 170 175

Ser Ser Thr Ile Val Ala Gln Ser Ala Lys Val Pro Cys Ile Pro Trp  
 180 185 190

Ser Gly Thr Gly Val Asp Thr Val His Val Asp Glu Lys Thr Gly Leu  
 195 200 205

Val Ser Val Asp Asp Asp Ile Tyr Gln Lys Gly Cys Cys Thr Ser Pro  
 210 215 220

Glu Asp Gly Leu Gln Lys Ala Lys Arg Ile Gly Phe Pro Val Met Ile  
 225 230 235 240

Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Gln Val Glu Arg  
 245 250 255

Glu Glu Asp Phe Ile Ala Leu Tyr His Gln Ala Ala Asn Glu Ile Pro  
 260 265 270

Gly Ser Pro Ile Phe Ile Met Lys Leu Ala Gly Arg Ala Arg His Leu  
 275 280 285

Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Thr Asn Ile Ser Leu Phe  
 290 295 300

Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile Ile Glu Glu  
 305 310 315 320

Ala Pro Val Thr Ile Ala Lys Ala Glu Thr Phe His Glu Met Glu Lys  
 325 330 335

Ala Ala Val Arg Leu Gly Lys Leu Val Gly Tyr Val Ser Ala Gly Thr  
 340 345 350

Val Glu Tyr Leu Tyr Ser His Asp Asp Gly Lys Phe Tyr Phe Leu Glu  
 355 360 365

Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr Thr Glu Met Val Ser  
 370 375 380

Gly Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala Met Gly Ile Pro  
 385 390 395 400

Met His Arg Ile Ser Asp Ile Arg Thr Leu Tyr Gly Met Asn Pro His  
 405 410 415

Ser Ala Ser Glu Ile Asp Phe Glu Phe Lys Thr Gln Asp Ala Thr Lys  
 420 425 430

Lys Gln Arg Arg Pro Ile Pro Lys Gly His Cys Thr Ala Cys Arg Ile  
 435 440 445

Thr Ser Glu Asp Pro Asn Asp Gly Phe Lys Pro Ser Gly Gly Thr Leu  
 450 455 460

His Glu Leu Asn Phe Arg Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser  
 465 470 475 480

Val Gly Asn Asn Gly Asn Ile His Ser Phe Ser Asp Ser Gln Phe Gly  
 485 490 495

His Ile Phe Ala Phe Gly Glu Asn Arg Gln Ala Ser Arg Lys His Met  
 500 505 510

Val Val Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr  
 515 520 525

Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Asp Phe Glu Asp Asn  
 530 535 540

Thr Ile Thr Thr Gly Trp Leu Asp Asp Leu Ile Thr His Lys Met Thr

560

<400> 46

Gly Asn Ala Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val  
165 170 175

Ala Gln Ser Ala Lys Val Pro Cys Ile Pro Trp Ser Gly Thr Gly Val  
180 185 190

Asp Thr Val His Val Asp Glu Lys Thr Gly Leu Val Ser Val Asp Asp  
195 200 205

Asp Ile Tyr Gln Lys Gly Cys Cys Thr Ser Pro Glu Asp Gly Leu Gln  
210 215 220

Lys Ala Lys Arg Ile Gly Phe Pro Val Met Ile Lys Ala Ser Glu Gly  
225 230 235 240

Gly Gly Gly Lys Gly Ile Arg Gln Val Glu Arg Glu Glu Asp Phe Ile  
245 250 255

Ala Leu Tyr His Gln Ala Ala Asn Glu Ile Pro Gly Ser Pro Ile Phe  
260 265 270

Ile Met Lys Leu Ala Gly Arg Ala Arg His Leu Glu Val Gln Leu Leu  
275 280 285

Ala Asp Gln Tyr Gly Thr Asn Ile Ser Leu Phe Gly Arg Asp Cys Ser  
290 295 300

Val Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala Pro Val Thr Ile  
305 310 315 320

Ala Lys Ala Glu Thr Phe His Glu Met Glu Lys Ala Ala Val Arg Leu  
325 330 335

Gly Lys Leu Val Gly Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr  
340 345 350

Ser His Asp Asp Gly Lys Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu  
355 360 365

Gln Val Glu His Pro Thr Thr Glu Met Val Ser Gly Val Asn Leu Pro  
370 375 380

Ala Ala Gln Leu Gln Ile Ala Met Gly Ile Pro Met His Arg Ile Ser  
385 390 395 400

Asp Ile Arg Thr Leu Tyr Gly Met Asn Pro His Ser Ala Ser Glu Ile  
405 410 415

Asp Phe Glu Phe Lys Thr Gln Asp Ala Thr Lys Lys Gln Arg Arg Pro



Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr  
 50 55 60

Phe Gly Asp Asp Arg Thr Val Gln Phe Val Ala Met Ala Thr Pro Glu  
 65 70 75 80

Asp Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met Ala Asp Gln Tyr Ile  
 85 90 95

Glu Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu  
 100 105 110

Ile Val Asp Ile Ala Glu Arg Ala Asp Val Asp Ala Val Trp Ala Gly  
 115 120 125

Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro Glu Lys Leu Ser Gln  
 130 135 140

Ser Lys Arg Lys Val Ile Phe Ile Gly Pro Pro Gly Asn Ala Met Arg  
 145 150 155 160

Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln Ser Ala Lys  
 165 170 175

Val Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp Thr Val His Val  
 180 185 190

Asp Glu Lys Thr Gly Leu Val Ser Val Asp Asp Asp Ile Tyr Gln Lys  
 195 200 205

Gly Cys Cys Thr Ser Pro Glu Asp Gly Leu Gln Lys Ala Lys Arg Ile  
 210 215 220

Gly Phe Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly  
 225 230 235 240

Ile Arg Gln Val Glu Arg Glu Glu Asp Phe Ile Ala Leu Tyr His Gln  
 245 250 255

Ala Ala Asn Glu Ile Pro Gly Ser Pro Ile Phe Ile Met Lys Leu Ala  
 260 265 270

Gly Arg Ala Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly  
 275 280 285

Thr Asn Ile Ser Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His

290	295	300
Gln Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala Lys Ala Glu Thr 305 310 315 320		
Phe His Glu Met Glu Lys Ala Ala Val Arg Leu Gly Lys Leu Val Gly 325 330 335		
Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser His Asp Asp Gly 340 345 350		
Lys Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro 355 360 365		
Thr Thr Glu Met Val Ser Gly Val Asn Leu Pro Ala Ala Gln Leu Gln 370 375 380		
Ile Ala Met Gly Ile Pro Met His Arg Ile Ser Asp Ile Arg Thr Leu 385 390 395 400		
Tyr Gly Met Asn Pro His Ser Ala Ser Glu Ile Asp Phe Glu Phe Lys 405 410 415		
Thr Gln Asp Ala Thr Lys Lys Gln Arg Arg Pro Ile Pro Lys Gly His 420 425 430		
Cys Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Asn Asp Gly Phe Lys 435 440 445		
Pro Ser Gly Gly Thr Leu His Glu Leu Asn Phe Arg Ser Ser Ser Asn 450 455 460		
Val Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly Asn Ile His Ser Phe 465 470 475 480		
Ser Asp Ser Gln Phe Gly His Ile Phe Ala Phe Gly Glu Asn Arg Gln 485 490 495		
Ala Ser Arg Lys His Met Val Val Ala Leu Lys Glu Leu Ser Ile Arg 500 505 510		
Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr 515 520 525		
Glu Asp Phe Glu Asp Asn Thr Ile Thr Thr Gly Trp 530 535 540		



<210> 48  
 <211> 545  
 <212> PRT  
 <213> Phytophthora infestans

<220>  
 <221> MISC\_FEATURE  
 <222> (1)..(545)  
 <223> N-terminal deleted Phytophthora ACCase BC domain (AAs 11-555)

<400> 48

Asp Val Ala Ala Tyr Ala Glu Thr Arg Ser Asp Ser Asn Pro Leu Asn  
 1 5 10 15

Tyr Ala Ser Met Glu Glu Tyr Val Arg Leu Gln Lys Gly Thr Arg Pro  
 20 25 30

Ile Thr Ser Val Leu Ile Ala Asn Asn Gly Ile Ser Ala Val Lys Ala  
 35 40 45

Ile Arg Ser Ile Arg Ser Trp Ser Tyr Glu Met Phe Ala Asp Glu His  
 50 55 60

Val Val Thr Phe Val Val Met Ala Thr Pro Glu Asp Leu Lys Ala Asn  
 65 70 75 80

Ala Glu Tyr Ile Arg Met Ala Glu His Val Val Glu Val Pro Gly Gly  
 85 90 95

Ser Asn Asn His Asn Tyr Ala Asn Val Ser Leu Ile Ile Glu Ile Ala  
 100 105 110

Glu Arg Phe Asn Val Asp Ala Val Trp Ala Gly Trp Gly His Ala Ser  
 115 120 125

Glu Asn Pro Leu Leu Pro Asp Thr Leu Ala Gln Thr Glu Arg Lys Ile  
 130 135 140

Val Phe Ile Gly Pro Pro Gly Lys Pro Met Arg Ala Leu Gly Asp Lys  
 145 150 155 160

Ile Gly Ser Thr Ile Ile Ala Gln Ser Ala Lys Val Pro Thr Ile Ala  
 165 170 175

Trp Asn Gly Asp Gly Met Glu Val Asp Tyr Lys Glu His Asp Gly Ile  
 180 185 190

Pro Asp Glu Ile Tyr Asn Ala Ala Met Leu Arg Asp Gly Gln His Cys  
 195 200 205

Leu Asp Glu Cys Lys Arg Ile Gly Phe Pro Val Met Ile Lys Ala Ser  
 210 215 220

Glu Gly Gly Gly Gly Lys Gly Ile Arg Met Val His Glu Glu Ser Gln  
 225 230 235 240

Val Leu Ser Ala Trp Glu Ala Val Arg Gly Glu Ile Pro Gly Ser Pro  
 245 250 255

Ile Phe Val Met Lys Leu Ala Pro Lys Ser Arg His Leu Glu Val Gln  
 260 265 270

Leu Leu Ala Asp Thr Tyr Gly Asn Ala Ile Ala Leu Ser Gly Arg Asp  
 275 280 285

Cys Ser Val Gln Arg Arg His Gln Lys Ile Val Glu Glu Gly Pro Val  
 290 295 300

Leu Ala Pro Thr Gln Glu Val Trp Glu Lys Met Met Arg Ala Ala Thr  
 305 310 315 320

Arg Leu Ala Gln Glu Val Glu Tyr Val Asn Ala Gly Thr Val Glu Tyr  
 325 330 335

Leu Phe Ser Glu Leu Pro Glu Asp Asn Gly Asn Ser Phe Phe Phe Leu  
 340 345 350

Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Val Thr Glu Met Ile  
 355 360 365

Thr His Val Asn Leu Pro Ala Ala Gln Leu Gln Val Ala Met Gly Ile  
 370 375 380

Pro Leu His Cys Ile Pro Asp Val Arg Arg Leu Tyr Asn Lys Asp Ala  
 385 390 395 400

Phe Glu Thr Thr Val Ile Asp Phe Asp Ala Glu Lys Gln Lys Pro Pro  
 405 410 415

His Gly His Val Ile Ala Ala Arg Ile Thr Ala Glu Asp Pro Asn Ala  
 420 425 430

Gly Phe Gln Pro Thr Ser Gly Ala Ile Gln Glu Leu Asn Phe Arg Ser  
435 440 445

Thr Pro Asp Val Trp Gly Tyr Phe Ser Val Asp Ser Ser Gly Gln Val  
450 455 460

His Glu Phe Ala Asp Ser Gln Ile Gly His Leu Phe Ser Trp Ser Pro  
465 470 475 480

Thr Arg Glu Lys Ala Arg Lys Asn Met Val Leu Ala Leu Lys Glu Leu  
485 490 495

Ser Ile Arg Gly Asp Ile His Thr Thr Val Glu Tyr Ile Val Asn Met  
500 505 510

Met Glu Ser Asp Asp Phe Lys Tyr Asn Arg Ile Ser Thr Ser Trp Leu  
515 520 525

Asp Glu Arg Ile Ser His His Asn Glu Val Arg Leu Gln Gly Arg Pro  
530 535 540

Asp  
545

<210> 49  
<211> 535  
<212> PRT  
<213> Phytophthora infestans

<220>  
<221> MISC\_FEATURE  
<222> (1)..(535)  
<223> N-terminal deleted Phytophthora ACCase BC domain (AAs 21-555)

<400> 49

Asp Ser Asn Pro Leu Asn Tyr Ala Ser Met Glu Glu Tyr Val Arg Leu  
1 5 10 15

Gln Lys Gly Thr Arg Pro Ile Thr Ser Val Leu Ile Ala Asn Asn Gly  
20 25 30

Ile Ser Ala Val Lys Ala Ile Arg Ser Ile Arg Ser Trp Ser Tyr Glu  
35 40 45

Met Phe Ala Asp Glu His Val Val Thr Phe Val Val Met Ala Thr Pro  
50 55 60

Glu Asp Leu Lys Ala Asn Ala Glu Tyr Ile Arg Met Ala Glu His Val  
 65 70 75 80

Val Glu Val Pro Gly Gly Ser Asn Asn His Asn Tyr Ala Asn Val Ser  
 85 90 95

Leu Ile Ile Glu Ile Ala Glu Arg Phe Asn Val Asp Ala Val Trp Ala  
 100 105 110

Gly Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro Asp Thr Leu Ala  
 115 120 125

Gln Thr Glu Arg Lys Ile Val Phe Ile Gly Pro Pro Gly Lys Pro Met  
 130 135 140

Arg Ala Leu Gly Asp Lys Ile Gly Ser Thr Ile Ile Ala Gln Ser Ala  
 145 150 155 160

Lys Val Pro Thr Ile Ala Trp Asn Gly Asp Gly Met Glu Val Asp Tyr  
 165 170 175

Lys Glu His Asp Gly Ile Pro Asp Glu Ile Tyr Asn Ala Ala Met Leu  
 180 185 190

Arg Asp Gly Gln His Cys Leu Asp Glu Cys Lys Arg Ile Gly Phe Pro  
 195 200 205

Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Met  
 210 215 220

Val His Glu Glu Ser Gln Val Leu Ser Ala Trp Glu Ala Val Arg Gly  
 225 230 235 240

Glu Ile Pro Gly Ser Pro Ile Phe Val Met Lys Leu Ala Pro Lys Ser  
 245 250 255

Arg His Leu Glu Val Gln Leu Leu Ala Asp Thr Tyr Gly Asn Ala Ile  
 260 265 270

Ala Leu Ser Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile  
 275 280 285

Val Glu Glu Gly Pro Val Leu Ala Pro Thr Gln Glu Val Trp Glu Lys  
 290 295 300

Met Met Arg Ala Ala Thr Arg Leu Ala Gln Glu Val Glu Tyr Val Asn  
 305 310 315 320

Ala Gly Thr Val Glu Tyr Leu Phe Ser Glu Leu Pro Glu Asp Asn Gly  
 325 330 335

Asn Ser Phe Phe Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His  
 340 345 350

Pro Val Thr Glu Met Ile Thr His Val Asn Leu Pro Ala Ala Gln Leu  
 355 360 365

Gln Val Ala Met Gly Ile Pro Leu His Cys Ile Pro Asp Val Arg Arg  
 370 375 380

Leu Tyr Asn Lys Asp Ala Phe Glu Thr Thr Val Ile Asp Phe Asp Ala  
 385 390 395 400

Glu Lys Gln Lys Pro Pro His Gly His Val Ile Ala Ala Arg Ile Thr  
 405 410 415

Ala Glu Asp Pro Asn Ala Gly Phe Gln Pro Thr Ser Gly Ala Ile Gln  
 420 425 430

Glu Leu Asn Phe Arg Ser Thr Pro Asp Val Trp Gly Tyr Phe Ser Val  
 435 440 445

Asp Ser Ser Gly Gln Val His Glu Phe Ala Asp Ser Gln Ile Gly His  
 450 455 460

Leu Phe Ser Trp Ser Pro Thr Arg Glu Lys Ala Arg Lys Asn Met Val  
 465 470 475 480

Leu Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Ile His Thr Thr Val  
 485 490 495

Glu Tyr Ile Val Asn Met Met Glu Ser Asp Asp Phe Lys Tyr Asn Arg  
 500 505 510

Ile Ser Thr Ser Trp Leu Asp Glu Arg Ile Ser His His Asn Glu Val  
 515 520 525

Arg Leu Gln Gly Arg Pro Asp  
 530 535

<210> 50

<211> 545  
 <212> PRT  
 <213> Phytophthora infestans

<220>  
 <221> MISC\_FEATURE  
 <222> (1)..(545)  
 <223> C-terminal deleted Phytophthora ACCase BC domain (AAs 1-545)

<400> 50

Met Val Ala Glu Glu Ala Pro Pro Ala Ala Asp Val Ala Ala Tyr Ala  
 1 5 10 15

Glu Thr Arg Ser Asp Ser Asn Pro Leu Asn Tyr Ala Ser Met Glu Glu  
 20 25 30

Tyr Val Arg Leu Gln Lys Gly Thr Arg Pro Ile Thr Ser Val Leu Ile  
 35 40 45

Ala Asn Asn Gly Ile Ser Ala Val Lys Ala Ile Arg Ser Ile Arg Ser  
 50 55 60

Trp Ser Tyr Glu Met Phe Ala Asp Glu His Val Val Thr Phe Val Val  
 65 70 75 80

Met Ala Thr Pro Glu Asp Leu Lys Ala Asn Ala Glu Tyr Ile Arg Met  
 85 90 95

Ala Glu His Val Val Glu Val Pro Gly Gly Ser Asn Asn His Asn Tyr  
 100 105 110

Ala Asn Val Ser Leu Ile Ile Glu Ile Ala Glu Arg Phe Asn Val Asp  
 115 120 125

Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro  
 130 135 140

Asp Thr Leu Ala Gln Thr Glu Arg Lys Ile Val Phe Ile Gly Pro Pro  
 145 150 155 160

Gly Lys Pro Met Arg Ala Leu Gly Asp Lys Ile Gly Ser Thr Ile Ile  
 165 170 175

Ala Gln Ser Ala Lys Val Pro Thr Ile Ala Trp Asn Gly Asp Gly Met  
 180 185 190

Glu Val Asp Tyr Lys Glu His Asp Gly Ile Pro Asp Glu Ile Tyr Asn

195	200	205																	
Ala	Ala	Met	Leu	Arg	Asp	Gly	Gln	His	Cys	Leu	Asp	Glu	Cys	Lys	Arg				
210						215					220								
Ile	Gly	Phe	Pro	Val	Met	Ile	Lys	Ala	Ser	Glu	Gly	Gly	Gly	Gly	Lys				
225					230					235					240				
Gly	Ile	Arg	Met	Val	His	Glu	Glu	Ser	Gln	Val	Leu	Ser	Ala	Trp	Glu				
				245					250					255					
Ala	Val	Arg	Gly	Glu	Ile	Pro	Gly	Ser	Pro	Ile	Phe	Val	Met	Lys	Leu				
			260					265					270						
Ala	Pro	Lys	Ser	Arg	His	Leu	Glu	Val	Gln	Leu	Leu	Ala	Asp	Thr	Tyr				
		275					280					285							
Gly	Asn	Ala	Ile	Ala	Leu	Ser	Gly	Arg	Asp	Cys	Ser	Val	Gln	Arg	Arg				
290						295					300								
His	Gln	Lys	Ile	Val	Glu	Glu	Gly	Pro	Val	Leu	Ala	Pro	Thr	Gln	Glu				
305					310					315					320				
Val	Trp	Glu	Lys	Met	Met	Arg	Ala	Ala	Thr	Arg	Leu	Ala	Gln	Glu	Val				
				325					330					335					
Glu	Tyr	Val	Asn	Ala	Gly	Thr	Val	Glu	Tyr	Leu	Phe	Ser	Glu	Leu	Pro				
			340					345					350						
Glu	Asp	Asn	Gly	Asn	Ser	Phe	Phe	Phe	Leu	Glu	Leu	Asn	Pro	Arg	Leu				
		355					360					365							
Gln	Val	Glu	His	Pro	Val	Thr	Glu	Met	Ile	Thr	His	Val	Asn	Leu	Pro				
370						375					380								
Ala	Ala	Gln	Leu	Gln	Val	Ala	Met	Gly	Ile	Pro	Leu	His	Cys	Ile	Pro				
385					390					395					400				
Asp	Val	Arg	Arg	Leu	Tyr	Asn	Lys	Asp	Ala	Phe	Glu	Thr	Thr	Val	Ile				
				405					410					415					
Asp	Phe	Asp	Ala	Glu	Lys	Gln	Lys	Pro	Pro	His	Gly	His	Val	Ile	Ala				
			420					425					430						
Ala	Arg	Ile	Thr	Ala	Glu	Asp	Pro	Asn	Ala	Gly	Phe	Gln	Pro	Thr	Ser				
		435					440					445							

Gly Ala Ile Gln Glu Leu Asn Phe Arg Ser Thr Pro Asp Val Trp Gly  
 450 455 460

Tyr Phe Ser Val Asp Ser Ser Gly Gln Val His Glu Phe Ala Asp Ser  
 465 470 475 480

Gln Ile Gly His Leu Phe Ser Trp Ser Pro Thr Arg Glu Lys Ala Arg  
 485 490 495

Lys Asn Met Val Leu Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Ile  
 500 505 510

His Thr Thr Val Glu Tyr Ile Val Asn Met Met Glu Ser Asp Asp Phe  
 515 520 525

Lys Tyr Asn Arg Ile Ser Thr Ser Trp Leu Asp Glu Arg Ile Ser His  
 530 535 540

His  
 545

<210> 51  
 <211> 535  
 <212> PRT  
 <213> Phytophthora infestans

<220>  
 <221> MISC\_FEATURE  
 <222> (1)..(535)  
 <223> C-terminal deleted Phytophthora ACCase BC domain (AAs 1-535)

<400> 51

Met Val Ala Glu Glu Ala Pro Pro Ala Ala Asp Val Ala Ala Tyr Ala  
 1 5 10 15

Glu Thr Arg Ser Asp Ser Asn Pro Leu Asn Tyr Ala Ser Met Glu Glu  
 20 25 30

Tyr Val Arg Leu Gln Lys Gly Thr Arg Pro Ile Thr Ser Val Leu Ile  
 35 40 45

Ala Asn Asn Gly Ile Ser Ala Val Lys Ala Ile Arg Ser Ile Arg Ser  
 50 55 60

Trp Ser Tyr Glu Met Phe Ala Asp Glu His Val Val Thr Phe Val Val  
 65 70 75 80



Met Ala Thr Pro Glu Asp Leu Lys Ala Asn Ala Glu Tyr Ile Arg Met  
 85 90 95

Ala Glu His Val Val Glu Val Pro Gly Gly Ser Asn Asn His Asn Tyr  
 100 105 110

Ala Asn Val Ser Leu Ile Ile Glu Ile Ala Glu Arg Phe Asn Val Asp  
 115 120 125

Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro  
 130 135 140

Asp Thr Leu Ala Gln Thr Glu Arg Lys Ile Val Phe Ile Gly Pro Pro  
 145 150 155 160

Gly Lys Pro Met Arg Ala Leu Gly Asp Lys Ile Gly Ser Thr Ile Ile  
 165 170 175

Ala Gln Ser Ala Lys Val Pro Thr Ile Ala Trp Asn Gly Asp Gly Met  
 180 185 190

Glu Val Asp Tyr Lys Glu His Asp Gly Ile Pro Asp Glu Ile Tyr Asn  
 195 200 205

Ala Ala Met Leu Arg Asp Gly Gln His Cys Leu Asp Glu Cys Lys Arg  
 210 215 220

Ile Gly Phe Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys  
 225 230 235 240

Gly Ile Arg Met Val His Glu Glu Ser Gln Val Leu Ser Ala Trp Glu  
 245 250 255

Ala Val Arg Gly Glu Ile Pro Gly Ser Pro Ile Phe Val Met Lys Leu  
 260 265 270

Ala Pro Lys Ser Arg His Leu Glu Val Gln Leu Leu Ala Asp Thr Tyr  
 275 280 285

Gly Asn Ala Ile Ala Leu Ser Gly Arg Asp Cys Ser Val Gln Arg Arg  
 290 295 300

His Gln Lys Ile Val Glu Glu Gly Pro Val Leu Ala Pro Thr Gln Glu  
 305 310 315 320

Val Trp Glu Lys Met Met Arg Ala Ala Thr Arg Leu Ala Gln Glu Val  
325 330 335

Glu Tyr Val Asn Ala Gly Thr Val Glu Tyr Leu Phe Ser Glu Leu Pro  
340 345 350

Glu Asp Asn Gly Asn Ser Phe Phe Phe Leu Glu Leu Asn Pro Arg Leu  
355 360 365

Gln Val Glu His Pro Val Thr Glu Met Ile Thr His Val Asn Leu Pro  
370 375 380

Ala Ala Gln Leu Gln Val Ala Met Gly Ile Pro Leu His Cys Ile Pro  
385 390 395 400

Asp Val Arg Arg Leu Tyr Asn Lys Asp Ala Phe Glu Thr Thr Val Ile  
405 410 415

Asp Phe Asp Ala Glu Lys Gln Lys Pro Pro His Gly His Val Ile Ala  
420 425 430

Ala Arg Ile Thr Ala Glu Asp Pro Asn Ala Gly Phe Gln Pro Thr Ser  
435 440 445

Gly Ala Ile Gln Glu Leu Asn Phe Arg Ser Thr Pro Asp Val Trp Gly  
450 455 460

Tyr Phe Ser Val Asp Ser Ser Gly Gln Val His Glu Phe Ala Asp Ser  
465 470 475 480

Gln Ile Gly His Leu Phe Ser Trp Ser Pro Thr Arg Glu Lys Ala Arg  
485 490 495

Lys Asn Met Val Leu Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Ile  
500 505 510

His Thr Thr Val Glu Tyr Ile Val Asn Met Met Glu Ser Asp Asp Phe  
515 520 525

Lys Tyr Asn Arg Ile Ser Thr  
530 535

<210> 52  
<211> 581  
<212> PRT  
<213> Magnaporthe grisea

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<220>
<221> MISC_FEATURE
<222> (1)..(581)
<223> N-terminal deleted Magnaporthe ACCase BC domain (AAs 12-592

<400> 52

Asn Ser Ser Arg Gln Arg Asn Gly Ala Asn Gly Val Thr Val Pro Val
1          5          10          15

Ala Asn Gly Lys Ala Thr Tyr Ala Gln Arg His Lys Ile Ala Asp His
20          25          30

Phe Ile Gly Gly Asn Arg Leu Glu Asn Ala Pro Pro Ser Lys Val Lys
35          40          45

Glu Trp Val Ala Ala His Asp Gly His Thr Val Ile Thr Asn Val Leu
50          55          60

Ile Ala Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Val Arg
65          70          75          80

Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu Arg Ala Ile Gln Phe Thr
85          90          95

Val Met Ala Thr Pro Glu Asp Leu Gln Ala Asn Ala Asp Tyr Ile Arg
100         105         110

Met Ala Asp His Tyr Val Glu Val Pro Gly Gly Thr Asn Asn Asn Asn
115         120         125

Tyr Ala Asn Val Glu Leu Ile Val Asp Val Ala Glu Arg Met Asn Val
130         135         140

His Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Lys Leu
145         150         155         160

Pro Glu Ser Leu Ala Ala Ser Pro Lys Lys Ile Ile Phe Ile Gly Pro
165         170         175

Pro Gly Ser Ala Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile
180         185         190

Val Ala Gln His Ala Gln Val Pro Cys Ile Pro Trp Ser Gly Thr Gly
195         200         205

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Val Asp Ala Val Gln Ile Asp Lys Lys Gly Ile Val Thr Val Asp Asp  
 210 215 220

Asp Thr Tyr Ala Lys Gly Cys Val Thr Ser Trp Gln Glu Gly Leu Glu  
 225 230 235 240

Lys Ala Arg Gln Ile Gly Phe Pro Val Met Ile Lys Ala Ser Glu Gly  
 245 250 255

Gly Gly Gly Lys Gly Ile Arg Lys Ala Val Ser Glu Glu Gly Phe Glu  
 260 265 270

Glu Leu Tyr Lys Ala Ala Ala Ser Glu Ile Pro Gly Ser Pro Ile Phe  
 275 280 285

Ile Met Lys Leu Ala Gly Asn Ala Arg His Leu Glu Val Gln Leu Leu  
 290 295 300

Ala Asp Gln Tyr Gly Asn Asn Ile Ser Leu Phe Gly Arg Asp Cys Ser  
 305 310 315 320

Val Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala Pro Val Thr Ile  
 325 330 335

Ala Lys Pro Asp Thr Phe Lys Ala Met Glu Glu Ala Ala Val Arg Leu  
 340 345 350

Gly Arg Leu Val Gly Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr  
 355 360 365

Ser His Ala Asp Asp Lys Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu  
 370 375 380

Gln Val Glu His Pro Thr Thr Glu Gly Val Ser Gly Val Asn Leu Pro  
 385 390 395 400

Ala Ser Gln Leu Gln Ile Ala Met Gly Ile Pro Leu His Arg Ile Ser  
 405 410 415

Asp Ile Arg Leu Leu Tyr Gly Val Asp Pro Lys Leu Ser Thr Glu Ile  
 420 425 430

Asp Phe Asp Phe Lys Asn Pro Asp Ser Glu Lys Thr Gln Arg Arg Pro  
 435 440 445

Ser Pro Lys Gly His Leu Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro

450                      455                      460  
 Gly Glu Gly Phe Lys Pro Ser Asn Gly Val Met His Glu Leu Asn Phe  
 465                      470                      475                      480  
 Arg Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val Gly Thr Gln Gly  
                     485                      490                      495  
 Gly Ile His Ser Phe Ser Asp Ser Gln Phe Gly His Ile Phe Ala Tyr  
                     500                      505                      510  
 Gly Glu Asn Arg Ser Ala Ser Arg Lys His Met Val Ile Ala Leu Lys  
                     515                      520                      525  
 Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile  
                     530                      535                      540  
 Lys Leu Leu Glu Thr Glu Ala Phe Glu Glu Asn Thr Ile Thr Thr Gly  
 545                      550                      555                      560  
 Trp Leu Asp Glu Leu Ile Ser Lys Lys Leu Thr Ala Glu Arg Pro Asp  
                     565                      570                      575  
 Lys Met Leu Ala Val  
                     580

<210> 53  
 <211> 571  
 <212> PRT  
 <213> Magnaporthe grisea

<220>  
 <221> MISC\_FEATURE  
 <222> (1)..(571)  
 <223> N-terminal deleted Magnaporthe ACCase BC domain (AAs 22-591)

<400> 53

Gly Val Thr Val Pro Val Ala Asn Gly Lys Ala Thr Tyr Ala Gln Arg  
 1                      5                      10                      15  
 His Lys Ile Ala Asp His Phe Ile Gly Gly Asn Arg Leu Glu Asn Ala  
                     20                      25                      30  
 Pro Pro Ser Lys Val Lys Glu Trp Val Ala Ala His Asp Gly His Thr  
                     35                      40                      45  
 Val Ile Thr Asn Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys

50		55		60
Glu Ile Arg Ser Val	Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu			
65	70	75		80
Arg Ala Ile Gln Phe Thr Val Met Ala Thr Pro Glu Asp Leu Gln Ala				
	85	90		95
Asn Ala Asp Tyr Ile Arg Met Ala Asp His Tyr Val Glu Val Pro Gly				
	100	105		110
Gly Thr Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Val Asp Val				
	115	120		125
Ala Glu Arg Met Asn Val His Ala Val Trp Ala Gly Trp Gly His Ala				
	130	135		140
Ser Glu Asn Pro Lys Leu Pro Glu Ser Leu Ala Ala Ser Pro Lys Lys				
145	150	155		160
Ile Ile Phe Ile Gly Pro Pro Gly Ser Ala Met Arg Ser Leu Gly Asp				
	165	170		175
Lys Ile Ser Ser Thr Ile Val Ala Gln His Ala Gln Val Pro Cys Ile				
	180	185		190
Pro Trp Ser Gly Thr Gly Val Asp Ala Val Gln Ile Asp Lys Lys Gly				
	195	200		205
Ile Val Thr Val Asp Asp Asp Thr Tyr Ala Lys Gly Cys Val Thr Ser				
	210	215		220
Trp Gln Glu Gly Leu Glu Lys Ala Arg Gln Ile Gly Phe Pro Val Met				
225	230	235		240
Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Lys Ala Val				
	245	250		255
Ser Glu Glu Gly Phe Glu Glu Leu Tyr Lys Ala Ala Ala Ser Glu Ile				
	260	265		270
Pro Gly Ser Pro Ile Phe Ile Met Lys Leu Ala Gly Asn Ala Arg His				
	275	280		285
Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn Asn Ile Ser Leu				
	290	295		300

Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile Ile Glu  
 305 310 315 320

Glu Ala Pro Val Thr Ile Ala Lys Pro Asp Thr Phe Lys Ala Met Glu  
 325 330 335

Glu Ala Ala Val Arg Leu Gly Arg Leu Val Gly Tyr Val Ser Ala Gly  
 340 345 350

Thr Val Glu Tyr Leu Tyr Ser His Ala Asp Asp Lys Phe Tyr Phe Leu  
 355 360 365

Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr Thr Glu Gly Val  
 370 375 380

Ser Gly Val Asn Leu Pro Ala Ser Gln Leu Gln Ile Ala Met Gly Ile  
 385 390 395 400

Pro Leu His Arg Ile Ser Asp Ile Arg Leu Leu Tyr Gly Val Asp Pro  
 405 410 415

Lys Leu Ser Thr Glu Ile Asp Phe Asp Phe Lys Asn Pro Asp Ser Glu  
 420 425 430

Lys Thr Gln Arg Arg Pro Ser Pro Lys Gly His Leu Thr Ala Cys Arg  
 435 440 445

Ile Thr Ser Glu Asp Pro Gly Glu Gly Phe Lys Pro Ser Asn Gly Val  
 450 455 460

Met His Glu Leu Asn Phe Arg Ser Ser Ser Asn Val Trp Gly Tyr Phe  
 465 470 475 480

Ser Val Gly Thr Gln Gly Gly Ile His Ser Phe Ser Asp Ser Gln Phe  
 485 490 495

Gly His Ile Phe Ala Tyr Gly Glu Asn Arg Ser Ala Ser Arg Lys His  
 500 505 510

Met Val Ile Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr  
 515 520 525

Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Ala Phe Glu Glu  
 530 535 540

Asn Thr Ile Thr Thr Gly Trp Leu Asp Glu Leu Ile Ser Lys Lys Leu  
 545 550 555 560

Thr Ala Glu Arg Pro Asp Lys Met Leu Ala Val  
 565 570

<210> 54  
 <211> 581  
 <212> PRT  
 <213> Magnaporthe grisea

<220>  
 <221> MISC\_FEATURE  
 <222> (1)..(581)  
 <223> C-terminal deleted Magnaporthe ACCase (AAs 2-582)

<400> 54

Thr Glu Thr Asn Gly Thr Ala Ala Ala Ala Asn Ser Ser Arg Gln Arg  
 1 5 10 15

Asn Gly Ala Asn Gly Val Thr Val Pro Val Ala Asn Gly Lys Ala Thr  
 20 25 30

Tyr Ala Gln Arg His Lys Ile Ala Asp His Phe Ile Gly Gly Asn Arg  
 35 40 45

Leu Glu Asn Ala Pro Pro Ser Lys Val Lys Glu Trp Val Ala Ala His  
 50 55 60

Asp Gly His Thr Val Ile Thr Asn Val Leu Ile Ala Asn Asn Gly Ile  
 65 70 75 80

Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr  
 85 90 95

Phe Gly Asp Glu Arg Ala Ile Gln Phe Thr Val Met Ala Thr Pro Glu  
 100 105 110

Asp Leu Gln Ala Asn Ala Asp Tyr Ile Arg Met Ala Asp His Tyr Val  
 115 120 125

Glu Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu  
 130 135 140

Ile Val Asp Val Ala Glu Arg Met Asn Val His Ala Val Trp Ala Gly  
 145 150 155 160



Trp Gly His Ala Ser Glu Asn Pro Lys Leu Pro Glu Ser Leu Ala Ala  
 165 170 175

Ser Pro Lys Lys Ile Ile Phe Ile Gly Pro Pro Gly Ser Ala Met Arg  
 180 185 190

Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln His Ala Gln  
 195 200 205

Val Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp Ala Val Gln Ile  
 210 215 220

Asp Lys Lys Gly Ile Val Thr Val Asp Asp Asp Thr Tyr Ala Lys Gly  
 225 230 235 240

Cys Val Thr Ser Trp Gln Glu Gly Leu Glu Lys Ala Arg Gln Ile Gly  
 245 250 255

Phe Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile  
 260 265 270

Arg Lys Ala Val Ser Glu Glu Gly Phe Glu Glu Leu Tyr Lys Ala Ala  
 275 280 285

Ala Ser Glu Ile Pro Gly Ser Pro Ile Phe Ile Met Lys Leu Ala Gly  
 290 295 300

Asn Ala Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn  
 305 310 315 320

Asn Ile Ser Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln  
 325 330 335

Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala Lys Pro Asp Thr Phe  
 340 345 350

Lys Ala Met Glu Glu Ala Ala Val Arg Leu Gly Arg Leu Val Gly Tyr  
 355 360 365

Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser His Ala Asp Asp Lys  
 370 375 380

Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr  
 385 390 395 400

Thr Glu Gly Val Ser Gly Val Asn Leu Pro Ala Ser Gln Leu Gln Ile  
 405 410 415  
 Ala Met Gly Ile Pro Leu His Arg Ile Ser Asp Ile Arg Leu Leu Tyr  
 420 425 430  
 Gly Val Asp Pro Lys Leu Ser Thr Glu Ile Asp Phe Asp Phe Lys Asn  
 435 440 445  
 Pro Asp Ser Glu Lys Thr Gln Arg Arg Pro Ser Pro Lys Gly His Leu  
 450 455 460  
 Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Gly Glu Gly Phe Lys Pro  
 465 470 475 480  
 Ser Asn Gly Val Met His Glu Leu Asn Phe Arg Ser Ser Ser Asn Val  
 485 490 495  
 Trp Gly Tyr Phe Ser Val Gly Thr Gln Gly Gly Ile His Ser Phe Ser  
 500 505 510  
 Asp Ser Gln Phe Gly His Ile Phe Ala Tyr Gly Glu Asn Arg Ser Ala  
 515 520 525  
 Ser Arg Lys His Met Val Ile Ala Leu Lys Glu Leu Ser Ile Arg Gly  
 530 535 540  
 Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu  
 545 550 555 560  
 Ala Phe Glu Glu Asn Thr Ile Thr Thr Gly Trp Leu Asp Glu Leu Ile  
 565 570 575  
 Ser Lys Lys Leu Thr  
 580  
 <210> 55  
 <211> 571  
 <212> PRT  
 <213> Magnaporthe grisea  
 <220>  
 <221> MISC\_FEATURE  
 <222> (1)..(571)  
 <223> C-terminal deleted Magnaporthe ACCase BC domain (AAs 2-572)  
 <400> 55

Thr Glu Thr Asn Gly Thr Ala Ala Ala Asn Ser Ser Arg Gln Arg  
 1 5 10 15  
 Asn Gly Ala Asn Gly Val Thr Val Pro Val Ala Asn Gly Lys Ala Thr  
 20 25 30  
 Tyr Ala Gln Arg His Lys Ile Ala Asp His Phe Ile Gly Gly Asn Arg  
 35 40 45  
 Leu Glu Asn Ala Pro Pro Ser Lys Val Lys Glu Trp Val Ala Ala His  
 50 55 60  
 Asp Gly His Thr Val Ile Thr Asn Val Leu Ile Ala Asn Asn Gly Ile  
 65 70 75 80  
 Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr  
 85 90 95  
 Phe Gly Asp Glu Arg Ala Ile Gln Phe Thr Val Met Ala Thr Pro Glu  
 100 105 110  
 Asp Leu Gln Ala Asn Ala Asp Tyr Ile Arg Met Ala Asp His Tyr Val  
 115 120 125  
 Glu Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu  
 130 135 140  
 Ile Val Asp Val Ala Glu Arg Met Asn Val His Ala Val Trp Ala Gly  
 145 150 155 160  
 Trp Gly His Ala Ser Glu Asn Pro Lys Leu Pro Glu Ser Leu Ala Ala  
 165 170 175  
 Ser Pro Lys Lys Ile Ile Phe Ile Gly Pro Pro Gly Ser Ala Met Arg  
 180 185 190  
 Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln His Ala Gln  
 195 200 205  
 Val Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp Ala Val Gln Ile  
 210 215 220  
 Asp Lys Lys Gly Ile Val Thr Val Asp Asp Asp Thr Tyr Ala Lys Gly  
 225 230 235 240  
 Cys Val Thr Ser Trp Gln Glu Gly Leu Glu Lys Ala Arg Gln Ile Gly

245					250					255					
Phe	Pro	Val	Met	Ile	Lys	Ala	Ser	Glu	Gly	Gly	Gly	Gly	Lys	Gly	Ile
			260					265					270		
Arg	Lys	Ala	Val	Ser	Glu	Glu	Gly	Phe	Glu	Glu	Leu	Tyr	Lys	Ala	Ala
			275					280					285		
Ala	Ser	Glu	Ile	Pro	Gly	Ser	Pro	Ile	Phe	Ile	Met	Lys	Leu	Ala	Gly
			290					295					300		
Asn	Ala	Arg	His	Leu	Glu	Val	Gln	Leu	Leu	Ala	Asp	Gln	Tyr	Gly	Asn
Asn	Ile	Ser	Leu	Phe	Gly	Arg	Asp	Cys	Ser	Val	Gln	Arg	Arg	His	Gln
Lys	Ile	Ile	Glu	Glu	Ala	Pro	Val	Thr	Ile	Ala	Lys	Pro	Asp	Thr	Phe
Lys	Ala	Met	Glu	Glu	Ala	Ala	Val	Arg	Leu	Gly	Arg	Leu	Val	Gly	Tyr
Val	Ser	Ala	Gly	Thr	Val	Glu	Tyr	Leu	Tyr	Ser	His	Ala	Asp	Asp	Lys
Phe	Tyr	Phe	Leu	Glu	Leu	Asn	Pro	Arg	Leu	Gln	Val	Glu	His	Pro	Thr
Thr	Glu	Gly	Val	Ser	Gly	Val	Asn	Leu	Pro	Ala	Ser	Gln	Leu	Gln	Ile
Ala	Met	Gly	Ile	Pro	Leu	His	Arg	Ile	Ser	Asp	Ile	Arg	Leu	Leu	Tyr
Gly	Val	Asp	Pro	Lys	Leu	Ser	Thr	Glu	Ile	Asp	Phe	Asp	Phe	Lys	Asn
Pro	Asp	Ser	Glu	Lys	Thr	Gln	Arg	Arg	Pro	Ser	Pro	Lys	Gly	His	Leu
Thr	Ala	Cys	Arg	Ile	Thr	Ser	Glu	Asp	Pro	Gly	Glu	Gly	Phe	Lys	Pro
Ser	Asn	Gly	Val	Met	His	Glu	Leu	Asn	Phe	Arg	Ser	Ser	Ser	Asn	Val

Trp Gly Tyr Phe Ser Val Gly Thr Gln Gly Gly Ile His Ser Phe Ser  
500 505 510

Asp Ser Gln Phe Gly His Ile Phe Ala Tyr Gly Glu Asn Arg Ser Ala  
515 520 525

Ser Arg Lys His Met Val Ile Ala Leu Lys Glu Leu Ser Ile Arg Gly  
530 535 540

Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu  
545 550 555 560

Ala Phe Glu Glu Asn Thr Ile Thr Thr Gly Trp  
565 570

<210> 56  
<211> 622  
<212> PRT  
<213> Homo sapiens

<220>  
<221> MISC\_FEATURE  
<222> (1)..(622)  
<223> C-terminal deleted Human ACCase1 BC domain (AAs 1-622)

<400> 56

Met Asp Glu Pro Ser Pro Leu Ala Gln Pro Leu Glu Leu Asn Gln His  
1 5 10 15

Ser Arg Phe Ile Ile Gly Ser Val Ser Glu Asp Asn Ser Glu Asp Glu  
20 25 30

Ile Ser Asn Leu Val Lys Leu Asp Leu Leu Glu Glu Lys Glu Gly Ser  
35 40 45

Leu Ser Pro Ala Ser Val Gly Ser Asp Thr Leu Ser Asp Leu Gly Ile  
50 55 60

Ser Ser Leu Gln Asp Gly Leu Ala Leu His Ile Arg Ser Ser Met Ser  
65 70 75 80

Gly Leu His Leu Val Lys Gln Gly Arg Asp Arg Lys Lys Ile Asp Ser  
85 90 95

Gln Arg Asp Phe Thr Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe  
100 105 110

Gly Gly Asn Lys Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile  
 115 120 125

Ala Ala Val Lys Cys Met Arg Ser Ile Arg Arg Trp Ser Tyr Glu Met  
 130 135 140

Phe Arg Asn Glu Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu  
 145 150 155 160

Asp Leu Lys Ala Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val  
 165 170 175

Pro Val Pro Gly Gly Pro Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu  
 180 185 190

Ile Leu Asp Ile Ala Lys Arg Ile Pro Val Gln Ala Val Trp Ala Gly  
 195 200 205

Trp Gly His Ala Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Lys  
 210 215 220

Asn Gly Ile Ala Phe Met Gly Pro Pro Ser Gln Ala Met Trp Ala Leu  
 225 230 235 240

Gly Asp Lys Ile Ala Ser Ser Ile Val Ala Gln Thr Ala Gly Ile Pro  
 245 250 255

Thr Leu Pro Trp Ser Gly Ser Gly Leu Arg Val Asp Trp Gln Glu Asn  
 260 265 270

Asp Phe Ser Lys Arg Ile Leu Asn Val Pro Gln Glu Leu Tyr Glu Lys  
 275 280 285

Gly Tyr Val Lys Asp Val Asp Asp Gly Leu Lys Ala Ala Glu Glu Val  
 290 295 300

Gly Tyr Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Lys Gly  
 305 310 315 320

Ile Arg Lys Val Asn Asn Ala Asp Asp Phe Pro Asn Leu Phe Arg Gln  
 325 330 335

Val Gln Ala Glu Val Pro Gly Ser Pro Ile Phe Val Met Arg Leu Ala  
 340 345 350

Lys Gln Ser Arg His Leu Glu Val Gln Ile Leu Ala Asp Gln Tyr Gly  
 355 360 365

Asn Ala Ile Ser Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His  
 370 375 380

Gln Lys Ile Ile Glu Glu Ala Pro Ala Thr Ile Ala Thr Pro Ala Val  
 385 390 395 400

Phe Glu His Met Glu Gln Cys Ala Val Lys Leu Ala Lys Met Val Gly  
 405 410 415

Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp Gly Ser  
 420 425 430

Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Cys  
 435 440 445

Thr Glu Met Val Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile  
 450 455 460

Ala Met Gly Ile Pro Leu Tyr Arg Ile Lys Asp Ile Arg Met Met Tyr  
 465 470 475 480

Gly Val Ser Pro Trp Gly Asp Ser Pro Ile Asp Phe Glu Asp Ser Ala  
 485 490 495

His Val Pro Cys Pro Arg Gly His Val Ile Ala Ala Arg Ile Thr Ser  
 500 505 510

Glu Asn Pro Asp Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu  
 515 520 525

Leu Asn Phe Arg Ser Asn Lys Asn Val Trp Gly Tyr Phe Ser Val Ala  
 530 535 540

Ala Ala Gly Gly Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys  
 545 550 555 560

Phe Ser Trp Gly Glu Asn Arg Glu Glu Ala Ile Ser Asn Met Val Val  
 565 570 575

Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu  
 580 585 590

Tyr Leu Ile Lys Leu Leu Glu Thr Glu Ser Phe Gln Met Asn Arg Ile  
595 600 605

Asp Thr Gly Trp Leu Asp Arg Leu Ile Ala Glu Lys Val Gln  
610 615 620

<210> 57  
<211> 612  
<212> PRT  
<213> Homo sapiens

<220>  
<221> MISC\_FEATURE  
<222> (1)..(612)  
<223> C-terminal deleted Human ACCase1 BC domain (AAs 1-612)

<400> 57

Met Asp Glu Pro Ser Pro Leu Ala Gln Pro Leu Glu Leu Asn Gln His  
1 5 10 15

Ser Arg Phe Ile Ile Gly Ser Val Ser Glu Asp Asn Ser Glu Asp Glu  
20 25 30

Ile Ser Asn Leu Val Lys Leu Asp Leu Leu Glu Glu Lys Glu Gly Ser  
35 40 45

Leu Ser Pro Ala Ser Val Gly Ser Asp Thr Leu Ser Asp Leu Gly Ile  
50 55 60

Ser Ser Leu Gln Asp Gly Leu Ala Leu His Ile Arg Ser Ser Met Ser  
65 70 75 80

Gly Leu His Leu Val Lys Gln Gly Arg Asp Arg Lys Lys Ile Asp Ser  
85 90 95

Gln Arg Asp Phe Thr Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe  
100 105 110

Gly Gly Asn Lys Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile  
115 120 125

Ala Ala Val Lys Cys Met Arg Ser Ile Arg Arg Trp Ser Tyr Glu Met  
130 135 140

Phe Arg Asn Glu Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu  
145 150 155 160



Asp Leu Lys Ala Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val  
 165 170 175

Pro Val Pro Gly Gly Pro Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu  
 180 185 190

Ile Leu Asp Ile Ala Lys Arg Ile Pro Val Gln Ala Val Trp Ala Gly  
 195 200 205

Trp Gly His Ala Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Leu Lys  
 210 215 220

Asn Gly Ile Ala Phe Met Gly Pro Pro Ser Gln Ala Met Trp Ala Leu  
 225 230 235 240

Gly Asp Lys Ile Ala Ser Ser Ile Val Ala Gln Thr Ala Gly Ile Pro  
 245 250 255

Thr Leu Pro Trp Ser Gly Ser Gly Leu Arg Val Asp Trp Gln Glu Asn  
 260 265 270

Asp Phe Ser Lys Arg Ile Leu Asn Val Pro Gln Glu Leu Tyr Glu Lys  
 275 280 285

Gly Tyr Val Lys Asp Val Asp Asp Gly Leu Lys Ala Ala Glu Glu Val  
 290 295 300

Gly Tyr Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly  
 305 310 315 320

Ile Arg Lys Val Asn Asn Ala Asp Asp Phe Pro Asn Leu Phe Arg Gln  
 325 330 335

Val Gln Ala Glu Val Pro Gly Ser Pro Ile Phe Val Met Arg Leu Ala  
 340 345 350

Lys Gln Ser Arg His Leu Glu Val Gln Ile Leu Ala Asp Gln Tyr Gly  
 355 360 365

Asn Ala Ile Ser Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His  
 370 375 380

Gln Lys Ile Ile Glu Glu Ala Pro Ala Thr Ile Ala Thr Pro Ala Val  
 385 390 395 400

Phe Glu His Met Glu Gln Cys Ala Val Lys Leu Ala Lys Met Val Gly

405										410					415				
Tyr	Val	Ser	Ala	Gly	Thr	Val	Glu	Tyr	Leu	Tyr	Ser	Gln	Asp	Gly	Ser				
			420					425					430						
Phe	Tyr	Phe	Leu	Glu	Leu	Asn	Pro	Arg	Leu	Gln	Val	Glu	His	Pro	Cys				
		435					440					445							
Thr	Glu	Met	Val	Ala	Asp	Val	Asn	Leu	Pro	Ala	Ala	Gln	Leu	Gln	Ile				
	450					455					460								
Ala	Met	Gly	Ile	Pro	Leu	Tyr	Arg	Ile	Lys	Asp	Ile	Arg	Met	Met	Tyr				
465					470					475					480				
Gly	Val	Ser	Pro	Trp	Gly	Asp	Ser	Pro	Ile	Asp	Phe	Glu	Asp	Ser	Ala				
				485					490					495					
His	Val	Pro	Cys	Pro	Arg	Gly	His	Val	Ile	Ala	Ala	Arg	Ile	Thr	Ser				
			500					505					510						
Glu	Asn	Pro	Asp	Glu	Gly	Phe	Lys	Pro	Ser	Ser	Gly	Thr	Val	Gln	Glu				
		515					520					525							
Leu	Asn	Phe	Arg	Ser	Asn	Lys	Asn	Val	Trp	Gly	Tyr	Phe	Ser	Val	Ala				
	530					535					540								
Ala	Ala	Gly	Gly	Leu	His	Glu	Phe	Ala	Asp	Ser	Gln	Phe	Gly	His	Cys				
545					550					555					560				
Phe	Ser	Trp	Gly	Glu	Asn	Arg	Glu	Glu	Ala	Ile	Ser	Asn	Met	Val	Val				
				565					570					575					
Ala	Leu	Lys	Glu	Leu	Ser	Ile	Arg	Gly	Asp	Phe	Arg	Thr	Thr	Val	Glu				
			580					585					590						
Tyr	Leu	Ile	Lys	Leu	Leu	Glu	Thr	Glu	Ser	Phe	Gln	Met	Asn	Arg	Ile				
		595					600					605							
Asp	Thr	Gly	Trp																
	610																		

<210> 58  
 <211> 522  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> MISC\_FEATURE  
 <222> (2)..(632)  
 <223> N- and C-terminal deleted Human ACCase1 (AAs 102-622)  
  
 <400> 58  
  
 Met Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe Gly Gly Asn Lys  
 1 5 10 15  
  
 Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys  
 20 25 30  
  
 Cys Met Arg Ser Ile Arg Arg Trp Ser Tyr Glu Met Phe Arg Asn Glu  
 35 40 45  
  
 Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu Asp Leu Lys Ala  
 50 55 60  
  
 Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val Pro Val Pro Gly  
 65 70 75 80  
  
 Gly Pro Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Leu Asp Ile  
 85 90 95  
  
 Ala Lys Arg Ile Pro Val Gln Ala Val Trp Ala Gly Trp Gly His Ala  
 100 105 110  
  
 Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Leu Lys Asn Gly Ile Ala  
 115 120 125  
  
 Phe Met Gly Pro Pro Ser Gln Ala Met Trp Ala Leu Gly Asp Lys Ile  
 130 135 140  
  
 Ala Ser Ser Ile Val Ala Gln Thr Ala Gly Ile Pro Thr Leu Pro Trp  
 145 150 155 160  
  
 Ser Gly Ser Gly Leu Arg Val Asp Trp Gln Glu Asn Asp Phe Ser Lys  
 165 170 175  
  
 Arg Ile Leu Asn Val Pro Gln Glu Leu Tyr Glu Lys Gly Tyr Val Lys  
 180 185 190  
  
 Asp Val Asp Asp Gly Leu Lys Ala Ala Glu Glu Val Gly Tyr Pro Val  
 195 200 205  
  
 Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Lys Val  
 210 215 220

Asn Asn Ala Asp Asp Phe Pro Asn Leu Phe Arg Gln Val Gln Ala Glu  
 225 230 235 240

Val Pro Gly Ser Pro Ile Phe Val Met Arg Leu Ala Lys Gln Ser Arg  
 245 250 255

His Leu Glu Val Gln Ile Leu Ala Asp Gln Tyr Gly Asn Ala Ile Ser  
 260 265 270

Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile Ile  
 275 280 285

Glu Glu Ala Pro Ala Thr Ile Ala Thr Pro Ala Val Phe Glu His Met  
 290 295 300

Glu Gln Cys Ala Val Lys Leu Ala Lys Met Val Gly Tyr Val Ser Ala  
 305 310 315 320

Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp Gly Ser Phe Tyr Phe Leu  
 325 330 335

Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Cys Thr Glu Met Val  
 340 345 350

Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala Met Gly Ile  
 355 360 365

Pro Leu Tyr Arg Ile Lys Asp Ile Arg Met Met Tyr Gly Val Ser Pro  
 370 375 380

Trp Gly Asp Ser Pro Ile Asp Phe Glu Asp Ser Ala His Val Pro Cys  
 385 390 395 400

Pro Arg Gly His Val Ile Ala Ala Arg Ile Thr Ser Glu Asn Pro Asp  
 405 410 415

Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu Leu Asn Phe Arg  
 420 425 430

Ser Asn Lys Asn Val Trp Gly Tyr Phe Ser Val Ala Ala Ala Gly Gly  
 435 440 445

Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys Phe Ser Trp Gly  
 450 455 460

Glu Asn Arg Glu Glu Ala Ile Ser Asn Met Val Val Ala Leu Lys Glu  
 465 470 475 480

Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys  
 485 490 495

Leu Leu Glu Thr Glu Ser Phe Gln Met Asn Arg Ile Asp Thr Gly Trp  
 500 505 510

Leu Asp Arg Leu Ile Ala Glu Lys Val Gln  
 515 520

<210> 59  
 <211> 512  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> MISC\_FEATURE  
 <222> (2)..(512)  
 <223> N- and C-terminal deleted Human ACCase1 BC domain (AAs 102-512)

<400> 59

Met Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe Gly Gly Asn Lys  
 1 5 10 15

Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys  
 20 25 30

Cys Met Arg Ser Ile Arg Arg Trp Ser Tyr Glu Met Phe Arg Asn Glu  
 35 40 45

Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu Asp Leu Lys Ala  
 50 55 60

Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val Pro Val Pro Gly  
 65 70 75 80

Gly Pro Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Leu Asp Ile  
 85 90 95

Ala Lys Arg Ile Pro Val Gln Ala Val Trp Ala Gly Trp Gly His Ala  
 100 105 110

Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Leu Lys Asn Gly Ile Ala  
 115 120 125

Phe Met Gly Pro Pro Ser Gln Ala Met Trp Ala Leu Gly Asp Lys Ile  
 130 135 140

Ala Ser Ser Ile Val Ala Gln Thr Ala Gly Ile Pro Thr Leu Pro Trp  
 145 150 155 160

Ser Gly Ser Gly Leu Arg Val Asp Trp Gln Glu Asn Asp Phe Ser Lys  
 165 170 175

Arg Ile Leu Asn Val Pro Gln Glu Leu Tyr Glu Lys Gly Tyr Val Lys  
 180 185 190

Asp Val Asp Asp Gly Leu Lys Ala Ala Glu Glu Val Gly Tyr Pro Val  
 195 200 205

Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Lys Val  
 210 215 220

Asn Asn Ala Asp Asp Phe Pro Asn Leu Phe Arg Gln Val Gln Ala Glu  
 225 230 235 240

Val Pro Gly Ser Pro Ile Phe Val Met Arg Leu Ala Lys Gln Ser Arg  
 245 250 255

His Leu Glu Val Gln Ile Leu Ala Asp Gln Tyr Gly Asn Ala Ile Ser  
 260 265 270

Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile Ile  
 275 280 285

Glu Glu Ala Pro Ala Thr Ile Ala Thr Pro Ala Val Phe Glu His Met  
 290 295 300

Glu Gln Cys Ala Val Lys Leu Ala Lys Met Val Gly Tyr Val Ser Ala  
 305 310 315 320

Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp Gly Ser Phe Tyr Phe Leu  
 325 330 335

Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Cys Thr Glu Met Val  
 340 345 350

Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala Met Gly Ile  
 355 360 365

Pro Leu Tyr Arg Ile Lys Asp Ile Arg Met Met Tyr Gly Val Ser Pro  
 370 375 380

Trp Gly Asp Ser Pro Ile Asp Phe Glu Asp Ser Ala His Val Pro Cys  
 385 390 395 400

Pro Arg Gly His Val Ile Ala Ala Arg Ile Thr Ser Glu Asn Pro Asp  
 405 410 415

Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu Leu Asn Phe Arg  
 420 425 430

Ser Asn Lys Asn Val Trp Gly Tyr Phe Ser Val Ala Ala Ala Gly Gly  
 435 440 445

Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys Phe Ser Trp Gly  
 450 455 460

Glu Asn Arg Glu Glu Ala Ile Ser Asn Met Val Val Ala Leu Lys Glu  
 465 470 475 480

Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys  
 485 490 495

Leu Leu Glu Thr Glu Ser Phe Gln Met Asn Arg Ile Asp Thr Gly Trp  
 500 505 510

<210> 60  
 <211> 764  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> MISC\_FEATURE  
 <222> (1)..(764)  
 <223> C-terminal deleted Human ACCase2 BC domain (AAs 1-764)

<400> 60

Met Val Leu Leu Leu Cys Leu Ser Cys Leu Ile Phe Ser Cys Leu Thr  
 1 5 10 15

Phe Ser Trp Leu Lys Ile Trp Gly Lys Met Thr Asp Ser Lys Pro Ile  
 20 25 30

Thr Lys Ser Lys Ser Glu Ala Asn Leu Ile Pro Ser Gln Glu Pro Phe  
 35 40 45

Pro Ala Ser Asp Asn Ser Gly Glu Thr Pro Gln Arg Asn Gly Glu Gly  
 50 55 60

His Thr Leu Pro Lys Thr Pro Ser Gln Ala Glu Pro Ala Ser His Lys  
 65 70 75 80

Gly Pro Lys Asp Ala Gly Arg Arg Arg Asn Ser Leu Pro Pro Ser His  
 85 90 95

Gln Lys Pro Pro Arg Asn Pro Leu Ser Ser Ser Asp Ala Ala Pro Ser  
 100 105 110

Pro Glu Leu Gln Ala Asn Gly Thr Gly Thr Gln Gly Leu Glu Ala Thr  
 115 120 125

Asp Thr Asn Gly Leu Ser Ser Ser Ala Arg Pro Gln Gly Gln Gln Ala  
 130 135 140

Gly Ser Pro Ser Lys Glu Asp Lys Lys Gln Ala Asn Ile Lys Arg Gln  
 145 150 155 160

Leu Met Thr Asn Phe Ile Leu Gly Ser Phe Asp Asp Tyr Ser Ser Asp  
 165 170 175

Glu Asp Ser Val Ala Gly Ser Ser Arg Glu Ser Thr Arg Lys Gly Ser  
 180 185 190

Arg Ala Ser Leu Gly Ala Leu Ser Leu Glu Ala Tyr Leu Thr Thr Gly  
 195 200 205

Glu Ala Glu Thr Arg Val Pro Thr Met Arg Pro Ser Met Ser Gly Leu  
 210 215 220

His Leu Val Lys Arg Gly Arg Glu His Lys Lys Leu Asp Leu His Arg  
 225 230 235 240

Asp Phe Thr Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe Gly Gly  
 245 250 255

Asp Arg Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile Ala Ala  
 260 265 270

Val Lys Cys Met Arg Ser Ile Arg Arg Trp Ala Tyr Glu Met Phe Arg  
 275 280 285

Asn Glu Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu Asp Leu



290	295	300
Lys Ala Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val Pro Val		
305	310	315 320
Pro Gly Gly Pro Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Val		
	325	330 335
Asp Ile Ala Lys Arg Ile Pro Leu Gln Ala Val Trp Ala Gly Trp Gly		
	340	345 350
His Ala Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Cys Lys Asn Gly		
	355	360 365
Val Ala Phe Leu Gly Pro Pro Ser Glu Ala Met Trp Ala Leu Gly Asp		
	370	375 380
Lys Ile Ala Ser Thr Val Val Ala Gln Thr Leu Gln Val Pro Thr Leu		
385	390	395 400
Pro Arg Ser Gly Ser Gly Leu Thr Val Glu Trp Thr Glu Asp Asp Leu		
	405	410 415
Gln Gln Gly Lys Arg Ile Ser Val Pro Glu Asp Val Tyr Asp Lys Gly		
	420	425 430
Cys Val Lys Asp Val Asp Glu Gly Leu Glu Ala Ala Glu Arg Ile Gly		
	435	440 445
Phe Pro Leu Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile		
	450	455 460
Arg Lys Ala Glu Ser Ala Glu Asp Phe Pro Ile Leu Phe Arg Gln Val		
465	470	475 480
Gln Ser Glu Ile Pro Gly Ser Pro Ile Phe Leu Met Lys Leu Ala Gln		
	485	490 495
His Ala Arg His Leu Glu Val Gln Ile Leu Ala Asp Gln Tyr Gly Asn		
	500	505 510
Ala Val Ser Leu Phe Gly Arg Asp Cys Ser Ile Gln Arg Arg His Gln		
	515	520 525
Lys Ile Val Glu Glu Ala Pro Ala Thr Ile Ala Pro Leu Ala Ile Phe		
530	535	540

Glu Phe Met Glu Gln Cys Ala Ile Arg Leu Ala Lys Thr Val Gly Tyr  
 545 550 555 560

Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp Gly Ser Phe  
 565 570 575

His Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Cys Thr  
 580 585 590

Glu Met Ile Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala  
 595 600 605

Met Gly Val Pro Leu His Arg Leu Lys Asp Ile Arg Leu Leu Tyr Gly  
 610 615 620

Glu Ser Pro Trp Gly Val Thr Pro Ile Ser Phe Glu Thr Pro Ser Asn  
 625 630 635 640

Pro Pro Leu Ala Arg Gly His Val Ile Ala Ala Arg Ile Thr Ser Glu  
 645 650 655

Asn Pro Asp Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu Leu  
 660 665 670

Asn Phe Arg Ser Ser Lys Asn Val Trp Gly Tyr Phe Ser Val Ala Ala  
 675 680 685

Thr Gly Gly Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys Phe  
 690 695 700

Ser Trp Gly Glu Asn Arg Lys Glu Ala Ile Ser Asn Met Val Val Ala  
 705 710 715 720

Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr  
 725 730 735

Leu Ile Asn Leu Leu Glu Thr Glu Ser Phe Gln Asn Asn Asp Ile Asp  
 740 745 750

Thr Gly Trp Leu Asp Tyr Leu Ile Ala Glu Lys Val  
 755 760

<210> 61  
 <211> 754  
 <212> PRT

<213> Homo sapiens

<220>

<221> MISC\_FEATURE

<222> (1)..(754)

<223> C-terminal deleted Human ACCase2 BC domain (AAs 1-754)

<400> 61

Met Val Leu Leu Leu Cys Leu Ser Cys Leu Ile Phe Ser Cys Leu Thr  
1 5 10 15

Phe Ser Trp Leu Lys Ile Trp Gly Lys Met Thr Asp Ser Lys Pro Ile  
20 25 30

Thr Lys Ser Lys Ser Glu Ala Asn Leu Ile Pro Ser Gln Glu Pro Phe  
35 40 45

Pro Ala Ser Asp Asn Ser Gly Glu Thr Pro Gln Arg Asn Gly Glu Gly  
50 55 60

His Thr Leu Pro Lys Thr Pro Ser Gln Ala Glu Pro Ala Ser His Lys  
65 70 75 80

Gly Pro Lys Asp Ala Gly Arg Arg Arg Asn Ser Leu Pro Pro Ser His  
85 90 95

Gln Lys Pro Pro Arg Asn Pro Leu Ser Ser Ser Asp Ala Ala Pro Ser  
100 105 110

Pro Glu Leu Gln Ala Asn Gly Thr Gly Thr Gln Gly Leu Glu Ala Thr  
115 120 125

Asp Thr Asn Gly Leu Ser Ser Ser Ala Arg Pro Gln Gly Gln Gln Ala  
130 135 140

Gly Ser Pro Ser Lys Glu Asp Lys Lys Gln Ala Asn Ile Lys Arg Gln  
145 150 155 160

Leu Met Thr Asn Phe Ile Leu Gly Ser Phe Asp Asp Tyr Ser Ser Asp  
165 170 175

Glu Asp Ser Val Ala Gly Ser Ser Arg Glu Ser Thr Arg Lys Gly Ser  
180 185 190

Arg Ala Ser Leu Gly Ala Leu Ser Leu Glu Ala Tyr Leu Thr Thr Gly  
195 200 205

Glu Ala Glu Thr Arg Val Pro Thr Met Arg Pro Ser Met Ser Gly Leu  
 210 215 220

His Leu Val Lys Arg Gly Arg Glu His Lys Lys Leu Asp Leu His Arg  
 225 230 235 240

Asp Phe Thr Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe Gly Gly  
 245 250 255

Asp Arg Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile Ala Ala  
 260 265 270

Val Lys Cys Met Arg Ser Ile Arg Arg Trp Ala Tyr Glu Met Phe Arg  
 275 280 285

Asn Glu Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu Asp Leu  
 290 295 300

Lys Ala Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val Pro Val  
 305 310 315 320

Pro Gly Gly Pro Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Val  
 325 330 335

Asp Ile Ala Lys Arg Ile Pro Leu Gln Ala Val Trp Ala Gly Trp Gly  
 340 345 350

His Ala Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Cys Lys Asn Gly  
 355 360 365

Val Ala Phe Leu Gly Pro Pro Ser Glu Ala Met Trp Ala Leu Gly Asp  
 370 375 380

Lys Ile Ala Ser Thr Val Val Ala Gln Thr Leu Gln Val Pro Thr Leu  
 385 390 395 400

Pro Arg Ser Gly Ser Gly Leu Thr Val Glu Trp Thr Glu Asp Asp Leu  
 405 410 415

Gln Gln Gly Lys Arg Ile Ser Val Pro Glu Asp Val Tyr Asp Lys Gly  
 420 425 430

Cys Val Lys Asp Val Asp Glu Gly Leu Glu Ala Ala Glu Arg Ile Gly  
 435 440 445

Phe Pro Leu Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile  
 450 455 460

Arg Lys Ala Glu Ser Ala Glu Asp Phe Pro Ile Leu Phe Arg Gln Val  
 465 470 475 480

Gln Ser Glu Ile Pro Gly Ser Pro Ile Phe Leu Met Lys Leu Ala Gln  
 485 490 495

His Ala Arg His Leu Glu Val Gln Ile Leu Ala Asp Gln Tyr Gly Asn  
 500 505 510

Ala Val Ser Leu Phe Gly Arg Asp Cys Ser Ile Gln Arg Arg His Gln  
 515 520 525

Lys Ile Val Glu Glu Ala Pro Ala Thr Ile Ala Pro Leu Ala Ile Phe  
 530 535 540

Glu Phe Met Glu Gln Cys Ala Ile Arg Leu Ala Lys Thr Val Gly Tyr  
 545 550 555 560

Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp Gly Ser Phe  
 565 570 575

His Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Cys Thr  
 580 585 590

Glu Met Ile Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala  
 595 600 605

Met Gly Val Pro Leu His Arg Leu Lys Asp Ile Arg Leu Leu Tyr Gly  
 610 615 620

Glu Ser Pro Trp Gly Val Thr Pro Ile Ser Phe Glu Thr Pro Ser Asn  
 625 630 635 640

Pro Pro Leu Ala Arg Gly His Val Ile Ala Ala Arg Ile Thr Ser Glu  
 645 650 655

Asn Pro Asp Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu Leu  
 660 665 670

Asn Phe Arg Ser Ser Lys Asn Val Trp Gly Tyr Phe Ser Val Ala Ala  
 675 680 685

Thr Gly Gly Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys Phe

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690                               695                               700

Ser Trp Gly Glu Asn Arg Lys Glu Ala Ile Ser Asn Met Val Val Ala
705                               710                               715                               720

Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr
725                               730                               735

Leu Ile Asn Leu Leu Glu Thr Glu Ser Phe Gln Asn Asn Asp Ile Asp
740                               745                               750

Thr Gly

<210> 62
<211> 522
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (2)..(522)
<223> N- and C-terminal Human ACCase2 BC domain (AAs 224-764)

<400> 62

Met Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe Gly Gly Asp Arg
1                               5                               10                               15

Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys
20                               25                               30

Cys Met Arg Ser Ile Arg Arg Trp Ala Tyr Glu Met Phe Arg Asn Glu
35                               40                               45

Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu Asp Leu Lys Ala
50                               55                               60

Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val Pro Val Pro Gly
65                               70                               75                               80

Gly Pro Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Val Asp Ile
85                               90                               95

Ala Lys Arg Ile Pro Leu Gln Ala Val Trp Ala Gly Trp Gly His Ala
100                              105                              110

Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Cys Lys Asn Gly Val Ala

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115	120	125
Phe Leu Gly Pro Pro Ser Glu Ala Met Trp Ala Leu Gly Asp Lys Ile		
130	135	140
Ala Ser Thr Val Val Ala Gln Thr Leu Gln Val Pro Thr Leu Pro Arg		
145	150	155
Ser Gly Ser Gly Leu Thr Val Glu Trp Thr Glu Asp Asp Leu Gln Gln		
	165	170
Gly Lys Arg Ile Ser Val Pro Glu Asp Val Tyr Asp Lys Gly Cys Val		
	180	185
Lys Asp Val Asp Glu Gly Leu Glu Ala Ala Glu Arg Ile Gly Phe Pro		
	195	200
Leu Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Lys		
	210	215
Ala Glu Ser Ala Glu Asp Phe Pro Ile Leu Phe Arg Gln Val Gln Ser		
225	230	235
Glu Ile Pro Gly Ser Pro Ile Phe Leu Met Lys Leu Ala Gln His Ala		
	245	250
Arg His Leu Glu Val Gln Ile Leu Ala Asp Gln Tyr Gly Asn Ala Val		
	260	265
Ser Leu Phe Gly Arg Asp Cys Ser Ile Gln Arg Arg His Gln Lys Ile		
	275	280
Val Glu Glu Ala Pro Ala Thr Ile Ala Pro Leu Ala Ile Phe Glu Phe		
	290	295
Met Glu Gln Cys Ala Ile Arg Leu Ala Lys Thr Val Gly Tyr Val Ser		
305	310	315
Ala Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp Gly Ser Phe His Phe		
	325	330
Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Cys Thr Glu Met		
	340	345
Ile Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala Met Gly		
	355	360

Val Pro Leu His Arg Leu Lys Asp Ile Arg Leu Leu Tyr Gly Glu Ser  
 370 375 380

Pro Trp Gly Val Thr Pro Ile Ser Phe Glu Thr Pro Ser Asn Pro Pro  
 385 390 395 400

Leu Ala Arg Gly His Val Ile Ala Ala Arg Ile Thr Ser Glu Asn Pro  
 405 410 415

Asp Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu Leu Asn Phe  
 420 425 430

Arg Ser Ser Lys Asn Val Trp Gly Tyr Phe Ser Val Ala Ala Thr Gly  
 435 440 445

Gly Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys Phe Ser Trp  
 450 455 460

Gly Glu Asn Arg Lys Glu Ala Ile Ser Asn Met Val Val Ala Leu Lys  
 465 470 475 480

Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile  
 485 490 495

Asn Leu Leu Glu Thr Glu Ser Phe Gln Asn Asn Asp Ile Asp Thr Gly  
 500 505 510

Trp Leu Asp Tyr Leu Ile Ala Glu Lys Val  
 515 520

<210> 63

<211> 512

<212> PRT

<213> Homo sapiens

<220>

<221> MIC\_FEATURE

<222> (2)..(512)

<223> N- and C-terminal deleted Human ACCase2 BC domain (AAs 224-754)

<400> 63

Met Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe Gly Gly Asp Arg  
 1 5 10 15

Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys  
 20 25 30



Cys Met Arg Ser Ile Arg Arg Trp Ala Tyr Glu Met Phe Arg Asn Glu  
 35 40 45

Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu Asp Leu Lys Ala  
 50 55 60

Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val Pro Val Pro Gly  
 65 70 75 80

Gly Pro Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Val Asp Ile  
 85 90 95

Ala Lys Arg Ile Pro Leu Gln Ala Val Trp Ala Gly Trp Gly His Ala  
 100 105 110

Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Cys Lys Asn Gly Val Ala  
 115 120 125

Phe Leu Gly Pro Pro Ser Glu Ala Met Trp Ala Leu Gly Asp Lys Ile  
 130 135 140

Ala Ser Thr Val Val Ala Gln Thr Leu Gln Val Pro Thr Leu Pro Arg  
 145 150 155 160

Ser Gly Ser Gly Leu Thr Val Glu Trp Thr Glu Asp Asp Leu Gln Gln  
 165 170 175

Gly Lys Arg Ile Ser Val Pro Glu Asp Val Tyr Asp Lys Gly Cys Val  
 180 185 190

Lys Asp Val Asp Glu Gly Leu Glu Ala Ala Glu Arg Ile Gly Phe Pro  
 195 200 205

Leu Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Lys  
 210 215 220

Ala Glu Ser Ala Glu Asp Phe Pro Ile Leu Phe Arg Gln Val Gln Ser  
 225 230 235 240

Glu Ile Pro Gly Ser Pro Ile Phe Leu Met Lys Leu Ala Gln His Ala  
 245 250 255

Arg His Leu Glu Val Gln Ile Leu Ala Asp Gln Tyr Gly Asn Ala Val  
 260 265 270

Ser Leu Phe Gly Arg Asp Cys Ser Ile Gln Arg Arg His Gln Lys Ile  
 275 280 285

Val Glu Glu Ala Pro Ala Thr Ile Ala Pro Leu Ala Ile Phe Glu Phe  
 290 295 300

Met Glu Gln Cys Ala Ile Arg Leu Ala Lys Thr Val Gly Tyr Val Ser  
 305 310 315 320

Ala Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp Gly Ser Phe His Phe  
 325 330 335

Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Cys Thr Glu Met  
 340 345 350

Ile Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala Met Gly  
 355 360 365

Val Pro Leu His Arg Leu Lys Asp Ile Arg Leu Leu Tyr Gly Glu Ser  
 370 375 380

Pro Trp Gly Val Thr Pro Ile Ser Phe Glu Thr Pro Ser Asn Pro Pro  
 385 390 395 400

Leu Ala Arg Gly His Val Ile Ala Ala Arg Ile Thr Ser Glu Asn Pro  
 405 410 415

Asp Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu Leu Asn Phe  
 420 425 430

Arg Ser Ser Lys Asn Val Trp Gly Tyr Phe Ser Val Ala Ala Thr Gly  
 435 440 445

Gly Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys Phe Ser Trp  
 450 455 460

Gly Glu Asn Arg Lys Glu Ala Ile Ser Asn Met Val Val Ala Leu Lys  
 465 470 475 480

Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile  
 485 490 495

Asn Leu Leu Glu Thr Glu Ser Phe Gln Asn Asn Asp Ile Asp Thr Gly  
 500 505 510

<210> 64  
 <211> 521  
 <212> PRT  
 <213> Magnaporthe grisea

<220>  
 <221> MISC\_FEATURE  
 <222> (1)..(521)  
 <223> N-terminal deleted Magnaporthe ACCase BC domain (AAs 72-592)

<400> 64

Thr Asn Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys Glu Ile  
 1 5 10 15

Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu Arg Ala  
 20 25 30

Ile Gln Phe Thr Val Met Ala Thr Pro Glu Asp Leu Gln Ala Asn Ala  
 35 40 45

Asp Tyr Ile Arg Met Ala Asp His Tyr Val Glu Val Pro Gly Gly Thr  
 50 55 60

Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Val Asp Val Ala Glu  
 65 70 75 80

Arg Met Asn Val His Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu  
 85 90 95

Asn Pro Lys Leu Pro Glu Ser Leu Ala Ala Ser Pro Lys Lys Ile Ile  
 100 105 110

Phe Ile Gly Pro Pro Gly Ser Ala Met Arg Ser Leu Gly Asp Lys Ile  
 115 120 125

Ser Ser Thr Ile Val Ala Gln His Ala Gln Val Pro Cys Ile Pro Trp  
 130 135 140

Ser Gly Thr Gly Val Asp Ala Val Gln Ile Asp Lys Lys Gly Ile Val  
 145 150 155 160

Thr Val Asp Asp Asp Thr Tyr Ala Lys Gly Cys Val Thr Ser Trp Gln  
 165 170 175

Glu Gly Leu Glu Lys Ala Arg Gln Ile Gly Phe Pro Val Met Ile Lys  
 180 185 190

Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Lys Ala Val Ser Glu  
 195 200 205

Glu Gly Phe Glu Glu Leu Tyr Lys Ala Ala Ala Ser Glu Ile Pro Gly  
 210 215 220

Ser Pro Ile Phe Ile Met Lys Leu Ala Gly Asn Ala Arg His Leu Glu  
 225 230 235 240

Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn Asn Ile Ser Leu Phe Gly  
 245 250 255

Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala  
 260 265 270

Pro Val Thr Ile Ala Lys Pro Asp Thr Phe Lys Ala Met Glu Glu Ala  
 275 280 285

Ala Val Arg Leu Gly Arg Leu Val Gly Tyr Val Ser Ala Gly Thr Val  
 290 295 300

Glu Tyr Leu Tyr Ser His Ala Asp Asp Lys Phe Tyr Phe Leu Glu Leu  
 305 310 315 320

Asn Pro Arg Leu Gln Val Glu His Pro Thr Thr Glu Gly Val Ser Gly  
 325 330 335

Val Asn Leu Pro Ala Ser Gln Leu Gln Ile Ala Met Gly Ile Pro Leu  
 340 345 350

His Arg Ile Ser Asp Ile Arg Leu Leu Tyr Gly Val Asp Pro Lys Leu  
 355 360 365

Ser Thr Glu Ile Asp Phe Asp Phe Lys Asn Pro Asp Ser Glu Lys Thr  
 370 375 380

Gln Arg Arg Pro Ser Pro Lys Gly His Leu Thr Ala Cys Arg Ile Thr  
 385 390 395 400

Ser Glu Asp Pro Gly Glu Gly Phe Lys Pro Ser Asn Gly Val Met His  
 405 410 415

Glu Leu Asn Phe Arg Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val  
 420 425 430

Gly Thr Gln Gly Gly Ile His Ser Phe Ser Asp Ser Gln Phe Gly His

435                      440                      445  
 Ile Phe Ala Tyr Gly Glu Asn Arg Ser Ala Ser Arg Lys His Met Val  
 450                      455                      460  
  
 Ile Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val  
 465                      470                      475                      480  
  
 Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Ala Phe Glu Glu Asn Thr  
 485                      490                      495  
  
 Ile Thr Thr Gly Trp Leu Asp Glu Leu Ile Ser Lys Lys Leu Thr Ala  
 500                      505                      510  
  
 Glu Arg Pro Asp Lys Met Leu Ala Val  
 515                      520  
  
 <210> 65  
 <211> 511  
 <212> PRT  
 <213> Magnaporthe grisea  
  
 <220>  
 <221> MISC\_FEATURE  
 <222> (1)..(511)  
 <223> N- and C-terminal deleted Magnaporthe ACCase BC domain (AAs  
 72-582)  
  
 <400> 65  
  
 Thr Asn Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys Glu Ile  
 1                      5                      10                      15  
  
 Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu Arg Ala  
 20                      25                      30  
  
 Ile Gln Phe Thr Val Met Ala Thr Pro Glu Asp Leu Gln Ala Asn Ala  
 35                      40                      45  
  
 Asp Tyr Ile Arg Met Ala Asp His Tyr Val Glu Val Pro Gly Gly Thr  
 50                      55                      60  
  
 Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Val Asp Val Ala Glu  
 65                      70                      75                      80  
  
 Arg Met Asn Val His Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu  
 85                      90                      95

Asn Pro Lys Leu Pro Glu Ser Leu Ala Ala Ser Pro Lys Lys Ile Ile  
 100 105 110

Phe Ile Gly Pro Pro Gly Ser Ala Met Arg Ser Leu Gly Asp Lys Ile  
 115 120 125

Ser Ser Thr Ile Val Ala Gln His Ala Gln Val Pro Cys Ile Pro Trp  
 130 135 140

Ser Gly Thr Gly Val Asp Ala Val Gln Ile Asp Lys Lys Gly Ile Val  
 145 150 155 160

Thr Val Asp Asp Asp Thr Tyr Ala Lys Gly Cys Val Thr Ser Trp Gln  
 165 170 175

Glu Gly Leu Glu Lys Ala Arg Gln Ile Gly Phe Pro Val Met Ile Lys  
 180 185 190

Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Lys Ala Val Ser Glu  
 195 200 205

Glu Gly Phe Glu Glu Leu Tyr Lys Ala Ala Ala Ser Glu Ile Pro Gly  
 210 215 220

Ser Pro Ile Phe Ile Met Lys Leu Ala Gly Asn Ala Arg His Leu Glu  
 225 230 235 240

Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn Asn Ile Ser Leu Phe Gly  
 245 250 255

Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala  
 260 265 270

Pro Val Thr Ile Ala Lys Pro Asp Thr Phe Lys Ala Met Glu Glu Ala  
 275 280 285

Ala Val Arg Leu Gly Arg Leu Val Gly Tyr Val Ser Ala Gly Thr Val  
 290 295 300

Glu Tyr Leu Tyr Ser His Ala Asp Asp Lys Phe Tyr Phe Leu Glu Leu  
 305 310 315 320

Asn Pro Arg Leu Gln Val Glu His Pro Thr Thr Glu Gly Val Ser Gly  
 325 330 335

Val Asn Leu Pro Ala Ser Gln Leu Gln Ile Ala Met Gly Ile Pro Leu

340	345	350
His Arg Ile Ser Asp Ile Arg Leu Leu Tyr Gly Val Asp Pro Lys Leu		
355	360	365
Ser Thr Glu Ile Asp Phe Asp Phe Lys Asn Pro Asp Ser Glu Lys Thr		
370	375	380
Gln Arg Arg Pro Ser Pro Lys Gly His Leu Thr Ala Cys Arg Ile Thr		
385	390	395
Ser Glu Asp Pro Gly Glu Gly Phe Lys Pro Ser Asn Gly Val Met His		
405	410	415
Glu Leu Asn Phe Arg Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val		
420	425	430
Gly Thr Gln Gly Gly Ile His Ser Phe Ser Asp Ser Gln Phe Gly His		
435	440	445
Ile Phe Ala Tyr Gly Glu Asn Arg Ser Ala Ser Arg Lys His Met Val		
450	455	460
Ile Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val		
465	470	475
Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Ala Phe Glu Glu Asn Thr		
485	490	495
Ile Thr Thr Gly Trp Leu Asp Glu Leu Ile Ser Lys Lys Leu Thr		
500	505	510

<210> 66  
 <211> 501  
 <212> PRT  
 <213> Magnaporthe grisea

<220>  
 <221> misc\_feature  
 <223> N- and C-terminal deleted Magnaporthe ACCase BC domain (AAs 72-572)

<400> 66

Thr Asn Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys Glu Ile
1 5 10 15

Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu Arg Ala

20										25					30				
Ile	Gln	Phe	Thr	Val	Met	Ala	Thr	Pro	Glu	Asp	Leu	Gln	Ala	Asn	Ala				
	35						40					45							
Asp	Tyr	Ile	Arg	Met	Ala	Asp	His	Tyr	Val	Glu	Val	Pro	Gly	Gly	Thr				
	50					55					60								
Asn	Asn	Asn	Asn	Tyr	Ala	Asn	Val	Glu	Leu	Ile	Val	Asp	Val	Ala	Glu				
65					70					75					80				
Arg	Met	Asn	Val	His	Ala	Val	Trp	Ala	Gly	Trp	Gly	His	Ala	Ser	Glu				
				85					90					95					
Asn	Pro	Lys	Leu	Pro	Glu	Ser	Leu	Ala	Ala	Ser	Pro	Lys	Lys	Ile	Ile				
			100					105					110						
Phe	Ile	Gly	Pro	Pro	Gly	Ser	Ala	Met	Arg	Ser	Leu	Gly	Asp	Lys	Ile				
		115					120					125							
Ser	Ser	Thr	Ile	Val	Ala	Gln	His	Ala	Gln	Val	Pro	Cys	Ile	Pro	Trp				
	130					135					140								
Ser	Gly	Thr	Gly	Val	Asp	Ala	Val	Gln	Ile	Asp	Lys	Lys	Gly	Ile	Val				
145					150					155					160				
Thr	Val	Asp	Asp	Asp	Thr	Tyr	Ala	Lys	Gly	Cys	Val	Thr	Ser	Trp	Gln				
				165					170					175					
Glu	Gly	Leu	Glu	Lys	Ala	Arg	Gln	Ile	Gly	Phe	Pro	Val	Met	Ile	Lys				
		180						185					190						
Ala	Ser	Glu	Gly	Gly	Gly	Gly	Lys	Gly	Ile	Arg	Lys	Ala	Val	Ser	Glu				
		195					200					205							
Glu	Gly	Phe	Glu	Glu	Leu	Tyr	Lys	Ala	Ala	Ala	Ser	Glu	Ile	Pro	Gly				
	210					215					220								
Ser	Pro	Ile	Phe	Ile	Met	Lys	Leu	Ala	Gly	Asn	Ala	Arg	His	Leu	Glu				
225					230					235					240				
Val	Gln	Leu	Leu	Ala	Asp	Gln	Tyr	Gly	Asn	Asn	Ile	Ser	Leu	Phe	Gly				
				245					250					255					
Arg	Asp	Cys	Ser	Val	Gln	Arg	Arg	His	Gln	Lys	Ile	Ile	Glu	Glu	Ala				
			260					265					270						



Pro Val Thr Ile Ala Lys Pro Asp Thr Phe Lys Ala Met Glu Glu Ala  
 275 280 285

Ala Val Arg Leu Gly Arg Leu Val Gly Tyr Val Ser Ala Gly Thr Val  
 290 295 300

Glu Tyr Leu Tyr Ser His Ala Asp Asp Lys Phe Tyr Phe Leu Glu Leu  
 305 310 315 320

Asn Pro Arg Leu Gln Val Glu His Pro Thr Thr Glu Gly Val Ser Gly  
 325 330 335

Val Asn Leu Pro Ala Ser Gln Leu Gln Ile Ala Met Gly Ile Pro Leu  
 340 345 350

His Arg Ile Ser Asp Ile Arg Leu Leu Tyr Gly Val Asp Pro Lys Leu  
 355 360 365

Ser Thr Glu Ile Asp Phe Asp Phe Lys Asn Pro Asp Ser Glu Lys Thr  
 370 375 380

Gln Arg Arg Pro Ser Pro Lys Gly His Leu Thr Ala Cys Arg Ile Thr  
 385 390 395 400

Ser Glu Asp Pro Gly Glu Gly Phe Lys Pro Ser Asn Gly Val Met His  
 405 410 415

Glu Leu Asn Phe Arg Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val  
 420 425 430

Gly Thr Gln Gly Gly Ile His Ser Phe Ser Asp Ser Gln Phe Gly His  
 435 440 445

Ile Phe Ala Tyr Gly Glu Asn Arg Ser Ala Ser Arg Lys His Met Val  
 450 455 460

Ile Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val  
 465 470 475 480

Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Ala Phe Glu Glu Asn Thr  
 485 490 495

Ile Thr Thr Gly Trp  
 500

<210> 67  
 <211> 491  
 <212> PRT  
 <213> Magnaporthe grisea

<220>  
 <221> MISC\_FEATURE  
 <222> (1)..(491)  
 <223> N- and C-terminal deleted ACCase BC domain (AAs 72-562)

<400> 67

Thr Asn Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys Glu Ile  
 1 5 10 15

Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu Arg Ala  
 20 25 30

Ile Gln Phe Thr Val Met Ala Thr Pro Glu Asp Leu Gln Ala Asn Ala  
 35 40 45

Asp Tyr Ile Arg Met Ala Asp His Tyr Val Glu Val Pro Gly Gly Thr  
 50 55 60

Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Val Asp Val Ala Glu  
 65 70 75 80

Arg Met Asn Val His Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu  
 85 90 95

Asn Pro Lys Leu Pro Glu Ser Leu Ala Ala Ser Pro Lys Lys Ile Ile  
 100 105 110

Phe Ile Gly Pro Pro Gly Ser Ala Met Arg Ser Leu Gly Asp Lys Ile  
 115 120 125

Ser Ser Thr Ile Val Ala Gln His Ala Gln Val Pro Cys Ile Pro Trp  
 130 135 140

Ser Gly Thr Gly Val Asp Ala Val Gln Ile Asp Lys Lys Gly Ile Val  
 145 150 155 160

Thr Val Asp Asp Asp Thr Tyr Ala Lys Gly Cys Val Thr Ser Trp Gln  
 165 170 175

Glu Gly Leu Glu Lys Ala Arg Gln Ile Gly Phe Pro Val Met Ile Lys  
 180 185 190

Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Lys Ala Val Ser Glu  
 195 200 205

Glu Gly Phe Glu Glu Leu Tyr Lys Ala Ala Ala Ser Glu Ile Pro Gly  
 210 215 220

Ser Pro Ile Phe Ile Met Lys Leu Ala Gly Asn Ala Arg His Leu Glu  
 225 230 235 240

Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn Asn Ile Ser Leu Phe Gly  
 245 250 255

Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala  
 260 265 270

Pro Val Thr Ile Ala Lys Pro Asp Thr Phe Lys Ala Met Glu Glu Ala  
 275 280 285

Ala Val Arg Leu Gly Arg Leu Val Gly Tyr Val Ser Ala Gly Thr Val  
 290 295 300

Glu Tyr Leu Tyr Ser His Ala Asp Asp Lys Phe Tyr Phe Leu Glu Leu  
 305 310 315 320

Asn Pro Arg Leu Gln Val Glu His Pro Thr Thr Glu Gly Val Ser Gly  
 325 330 335

Val Asn Leu Pro Ala Ser Gln Leu Gln Ile Ala Met Gly Ile Pro Leu  
 340 345 350

His Arg Ile Ser Asp Ile Arg Leu Leu Tyr Gly Val Asp Pro Lys Leu  
 355 360 365

Ser Thr Glu Ile Asp Phe Asp Phe Lys Asn Pro Asp Ser Glu Lys Thr  
 370 375 380

Gln Arg Arg Pro Ser Pro Lys Gly His Leu Thr Ala Cys Arg Ile Thr  
 385 390 395 400

Ser Glu Asp Pro Gly Glu Gly Phe Lys Pro Ser Asn Gly Val Met His  
 405 410 415

Glu Leu Asn Phe Arg Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val  
 420 425 430

Gly Thr Gln Gly Gly Ile His Ser Phe Ser Asp Ser Gln Phe Gly His  
 435 440 445

Ile Phe Ala Tyr Gly Glu Asn Arg Ser Ala Ser Arg Lys His Met Val  
 450 455 460

Ile Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val  
 465 470 475 480

Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Ala  
 485 490

<210> 68  
 <211> 525  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<220>  
 <221> MISC\_FEATURE  
 <222> (1)..(525)  
 <223> N-terminal deleted Yeast ACCase BC domain (AAs--57-581)

<400> 68

Thr Val Ile Ser Lys Ile Leu Ile Ala Asn Asn Gly Ile Ala Ala Val  
 1 5 10 15

Lys Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp  
 20 25 30

Asp Arg Thr Val Gln Phe Val Ala Met Ala Thr Pro Glu Asp Leu Glu  
 35 40 45

Ala Asn Ala Glu Tyr Ile Arg Met Ala Asp Gln Tyr Ile Glu Val Pro  
 50 55 60

Gly Gly Thr Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile Val Asp  
 65 70 75 80

Ile Ala Glu Arg Ala Asp Val Asp Ala Val Trp Ala Gly Trp Gly His  
 85 90 95

Ala Ser Glu Asn Pro Leu Leu Pro Glu Lys Leu Ser Gln Ser Lys Arg  
 100 105 110

Lys Val Ile Phe Ile Gly Pro Pro Gly Asn Ala Met Arg Ser Leu Gly  
 115 120 125

Asp Lys Ile Ser Ser Thr Ile Val Ala Gln Ser Ala Lys Val Pro Cys  
 130 135 140

Ile Pro Trp Ser Gly Thr Gly Val Asp Thr Val His Val Asp Glu Lys  
 145 150 155 160

Thr Gly Leu Val Ser Val Asp Asp Asp Ile Tyr Gln Lys Gly Cys Cys  
 165 170 175

Thr Ser Pro Glu Asp Gly Leu Gln Lys Ala Lys Arg Ile Gly Phe Pro  
 180 185 190

Val Met Ile Lys Ala Ser Glu Gly Gly Gly Lys Gly Ile Arg Gln  
 195 200 205

Val Glu Arg Glu Glu Asp Phe Ile Ala Leu Tyr His Gln Ala Ala Asn  
 210 215 220

Glu Ile Pro Gly Ser Pro Ile Phe Ile Met Lys Leu Ala Gly Arg Ala  
 225 230 235 240

Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Thr Asn Ile  
 245 250 255

Ser Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile  
 260 265 270

Ile Glu Glu Ala Pro Val Thr Ile Ala Lys Ala Glu Thr Phe His Glu  
 275 280 285

Met Glu Lys Ala Ala Val Arg Leu Gly Lys Leu Val Gly Tyr Val Ser  
 290 295 300

Ala Gly Thr Val Glu Tyr Leu Tyr Ser His Asp Asp Gly Lys Phe Tyr  
 305 310 315 320

Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr Thr Glu  
 325 330 335

Met Val Ser Gly Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala Met  
 340 345 350

Gly Ile Pro Met His Arg Ile Ser Asp Ile Arg Thr Leu Tyr Gly Met  
 355 360 365

Asn Pro His Ser Ala Ser Glu Ile Asp Phe Glu Phe Lys Thr Gln Asp

370                                      375                                      380  
 Ala Thr Lys Lys Gln Arg Arg Pro Ile Pro Lys Gly His Cys Thr Ala  
 385                                      390                                      395                                      400  
 Cys Arg Ile Thr Ser Glu Asp Pro Asn Asp Gly Phe Lys Pro Ser Gly  
                                     405                                      410                                      415  
 Gly Thr Leu His Glu Leu Asn Phe Arg Ser Ser Ser Asn Val Trp Gly  
                                     420                                      425                                      430  
 Tyr Phe Ser Val Gly Asn Asn Gly Asn Ile His Ser Phe Ser Asp Ser  
                                     435                                      440                                      445  
 Gln Phe Gly His Ile Phe Ala Phe Gly Glu Asn Arg Gln Ala Ser Arg  
                                     450                                      455                                      460  
 Lys His Met Val Val Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe  
 465                                      470                                      475                                      480  
 Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Asp Phe  
                                     485                                      490                                      495  
 Glu Asp Asn Thr Ile Thr Thr Gly Trp Leu Asp Asp Leu Ile Thr His  
                                     500                                      505                                      510  
 Lys Met Thr Ala Glu Lys Pro Asp Pro Thr Leu Ala Val  
                                     515                                      520                                      525  
  
 <210> 69  
 <211> 515  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*  
  
 <220>  
 <221> MISC\_FEATURE  
 <222> (1)..(515)  
 <223> N- and C-terminal deleted Yeast ACCase BC domain (AAs 57-571)  
  
 <400> 69  
  
 Thr Val Ile Ser Lys Ile Leu Ile Ala Asn Asn Gly Ile Ala Ala Val  
 1                                      5                                      10                                      15  
  
 Lys Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp  
                                     20                                      25                                      30  
  
 Asp Arg Thr Val Gln Phe Val Ala Met Ala Thr Pro Glu Asp Leu Glu

35

40

45

Ala Asn Ala Glu Tyr Ile Arg Met Ala Asp Gln Tyr Ile Glu Val Pro  
 50 55 60

Gly Gly Thr Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile Val Asp  
 65 70 75 80

Ile Ala Glu Arg Ala Asp Val Asp Ala Val Trp Ala Gly Trp Gly His  
 85 90 95

Ala Ser Glu Asn Pro Leu Leu Pro Glu Lys Leu Ser Gln Ser Lys Arg  
 100 105 110

Lys Val Ile Phe Ile Gly Pro Pro Gly Asn Ala Met Arg Ser Leu Gly  
 115 120 125

Asp Lys Ile Ser Ser Thr Ile Val Ala Gln Ser Ala Lys Val Pro Cys  
 130 135 140

Ile Pro Trp Ser Gly Thr Gly Val Asp Thr Val His Val Asp Glu Lys  
 145 150 155 160

Thr Gly Leu Val Ser Val Asp Asp Asp Ile Tyr Gln Lys Gly Cys Cys  
 165 170 175

Thr Ser Pro Glu Asp Gly Leu Gln Lys Ala Lys Arg Ile Gly Phe Pro  
 180 185 190

Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Gln  
 195 200 205

Val Glu Arg Glu Glu Asp Phe Ile Ala Leu Tyr His Gln Ala Ala Asn  
 210 215 220

Glu Ile Pro Gly Ser Pro Ile Phe Ile Met Lys Leu Ala Gly Arg Ala  
 225 230 235 240

Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Thr Asn Ile  
 245 250 255

Ser Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile  
 260 265 270

Ile Glu Glu Ala Pro Val Thr Ile Ala Lys Ala Glu Thr Phe His Glu  
 275 280 285

Met Glu Lys Ala Ala Val Arg Leu Gly Lys Leu Val Gly Tyr Val Ser  
 290 295 300

Ala Gly Thr Val Glu Tyr Leu Tyr Ser His Asp Asp Gly Lys Phe Tyr  
 305 310 315 320

Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr Thr Glu  
 325 330 335

Met Val Ser Gly Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala Met  
 340 345 350

Gly Ile Pro Met His Arg Ile Ser Asp Ile Arg Thr Leu Tyr Gly Met  
 355 360 365

Asn Pro His Ser Ala Ser Glu Ile Asp Phe Glu Phe Lys Thr Gln Asp  
 370 375 380

Ala Thr Lys Lys Gln Arg Arg Pro Ile Pro Lys Gly His Cys Thr Ala  
 385 390 395 400

Cys Arg Ile Thr Ser Glu Asp Pro Asn Asp Gly Phe Lys Pro Ser Gly  
 405 410 415

Gly Thr Leu His Glu Leu Asn Phe Arg Ser Ser Ser Asn Val Trp Gly  
 420 425 430

Tyr Phe Ser Val Gly Asn Asn Gly Asn Ile His Ser Phe Ser Asp Ser  
 435 440 445

Gln Phe Gly His Ile Phe Ala Phe Gly Glu Asn Arg Gln Ala Ser Arg  
 450 455 460

Lys His Met Val Val Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe  
 465 470 475 480

Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Asp Phe  
 485 490 495

Glu Asp Asn Thr Ile Thr Thr Gly Trp Leu Asp Asp Leu Ile Thr His  
 500 505 510

Lys Met Thr  
 515



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<210> 70
<211> 505
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> MISC_FEATURE
<222> (1)..(505)
<223> N- and C-terminal deleted Yeast ACCase BC domain (AAs 57-561)

<400> 70

Thr Val Ile Ser Lys Ile Leu Ile Ala Asn Asn Gly Ile Ala Ala Val
1          5          10          15

Lys Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp
          20          25          30

Asp Arg Thr Val Gln Phe Val Ala Met Ala Thr Pro Glu Asp Leu Glu
          35          40          45

Ala Asn Ala Glu Tyr Ile Arg Met Ala Asp Gln Tyr Ile Glu Val Pro
          50          55          60

Gly Gly Thr Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile Val Asp
65          70          75          80

Ile Ala Glu Arg Ala Asp Val Asp Ala Val Trp Ala Gly Trp Gly His
          85          90          95

Ala Ser Glu Asn Pro Leu Leu Pro Glu Lys Leu Ser Gln Ser Lys Arg
          100          105          110

Lys Val Ile Phe Ile Gly Pro Pro Gly Asn Ala Met Arg Ser Leu Gly
          115          120          125

Asp Lys Ile Ser Ser Thr Ile Val Ala Gln Ser Ala Lys Val Pro Cys
          130          135          140

Ile Pro Trp Ser Gly Thr Gly Val Asp Thr Val His Val Asp Glu Lys
145          150          155          160

Thr Gly Leu Val Ser Val Asp Asp Asp Ile Tyr Gln Lys Gly Cys Cys
          165          170          175

Thr Ser Pro Glu Asp Gly Leu Gln Lys Ala Lys Arg Ile Gly Phe Pro
          180          185          190

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Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Gln  
195 200 205

Val Glu Arg Glu Glu Asp Phe Ile Ala Leu Tyr His Gln Ala Ala Asn  
210 215 220

Glu Ile Pro Gly Ser Pro Ile Phe Ile Met Lys Leu Ala Gly Arg Ala  
225 230 235 240

Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Thr Asn Ile  
245 250 255

Ser Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile  
260 265 270

Ile Glu Glu Ala Pro Val Thr Ile Ala Lys Ala Glu Thr Phe His Glu  
275 280 285

Met Glu Lys Ala Ala Val Arg Leu Gly Lys Leu Val Gly Tyr Val Ser  
290 295 300

Ala Gly Thr Val Glu Tyr Leu Tyr Ser His Asp Asp Gly Lys Phe Tyr  
305 310 315 320

Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr Thr Glu  
325 330 335

Met Val Ser Gly Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala Met  
340 345 350

Gly Ile Pro Met His Arg Ile Ser Asp Ile Arg Thr Leu Tyr Gly Met  
355 360 365

Asn Pro His Ser Ala Ser Glu Ile Asp Phe Glu Phe Lys Thr Gln Asp  
370 375 380

Ala Thr Lys Lys Gln Arg Arg Pro Ile Pro Lys Gly His Cys Thr Ala  
385 390 395 400

Cys Arg Ile Thr Ser Glu Asp Pro Asn Asp Gly Phe Lys Pro Ser Gly  
405 410 415

Gly Thr Leu His Glu Leu Asn Phe Arg Ser Ser Ser Asn Val Trp Gly  
420 425 430

Tyr Phe Ser Val Gly Asn Asn Gly Asn Ile His Ser Phe Ser Asp Ser  
435 440 445

Gln Phe Gly His Ile Phe Ala Phe Gly Glu Asn Arg Gln Ala Ser Arg  
450 455 460

Lys His Met Val Val Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe  
465 470 475 480

Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Asp Phe  
485 490 495

Glu Asp Asn Thr Ile Thr Thr Gly Trp  
500 505

<210> 71  
<211> 495  
<212> PRT  
<213> *Saccharomyces cerevisiae*

<220>  
<221> MISC\_FEATURE  
<222> (1)..(495)  
<223> N- and C-terminal deleted YEast ACCase BC domain (AAs 57-551)  
<400> 71

Thr Val Ile Ser Lys Ile Leu Ile Ala Asn Asn Gly Ile Ala Ala Val  
1 5 10 15

Lys Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp  
20 25 30

Asp Arg Thr Val Gln Phe Val Ala Met Ala Thr Pro Glu Asp Leu Glu  
35 40 45

Ala Asn Ala Glu Tyr Ile Arg Met Ala Asp Gln Tyr Ile Glu Val Pro  
50 55 60

Gly Gly Thr Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile Val Asp  
65 70 75 80

Ile Ala Glu Arg Ala Asp Val Asp Ala Val Trp Ala Gly Trp Gly His  
85 90 95

Ala Ser Glu Asn Pro Leu Leu Pro Glu Lys Leu Ser Gln Ser Lys Arg  
100 105 110

Lys Val Ile Phe Ile Gly Pro Pro Gly Asn Ala Met Arg Ser Leu Gly  
 115 120 125

Asp Lys Ile Ser Ser Thr Ile Val Ala Gln Ser Ala Lys Val Pro Cys  
 130 135 140

Ile Pro Trp Ser Gly Thr Gly Val Asp Thr Val His Val Asp Glu Lys  
 145 150 155 160

Thr Gly Leu Val Ser Val Asp Asp Asp Ile Tyr Gln Lys Gly Cys Cys  
 165 170 175

Thr Ser Pro Glu Asp Gly Leu Gln Lys Ala Lys Arg Ile Gly Phe Pro  
 180 185 190

Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Gln  
 195 200 205

Val Glu Arg Glu Glu Asp Phe Ile Ala Leu Tyr His Gln Ala Ala Asn  
 210 215 220

Glu Ile Pro Gly Ser Pro Ile Phe Ile Met Lys Leu Ala Gly Arg Ala  
 225 230 235 240

Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Thr Asn Ile  
 245 250 255

Ser Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile  
 260 265 270

Ile Glu Glu Ala Pro Val Thr Ile Ala Lys Ala Glu Thr Phe His Glu  
 275 280 285

Met Glu Lys Ala Ala Val Arg Leu Gly Lys Leu Val Gly Tyr Val Ser  
 290 295 300

Ala Gly Thr Val Glu Tyr Leu Tyr Ser His Asp Asp Gly Lys Phe Tyr  
 305 310 315 320

Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr Thr Glu  
 325 330 335

Met Val Ser Gly Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala Met  
 340 345 350

Gly Ile Pro Met His Arg Ile Ser Asp Ile Arg Thr Leu Tyr Gly Met

355	360	365
Asn Pro His Ser Ala Ser Glu Ile Asp Phe Glu Phe Lys Thr Gln Asp		
370	375	380
Ala Thr Lys Lys Gln Arg Arg Pro Ile Pro Lys Gly His Cys Thr Ala		
385	390	395
Cys Arg Ile Thr Ser Glu Asp Pro Asn Asp Gly Phe Lys Pro Ser Gly		
405	410	415
Gly Thr Leu His Glu Leu Asn Phe Arg Ser Ser Ser Asn Val Trp Gly		
420	425	430
Tyr Phe Ser Val Gly Asn Asn Gly Asn Ile His Ser Phe Ser Asp Ser		
435	440	445
Gln Phe Gly His Ile Phe Ala Phe Gly Glu Asn Arg Gln Ala Ser Arg		
450	455	460
Lys His Met Val Val Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe		
465	470	475
Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Asp		
485	490	495